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Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Perfect score:
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seq length: 2000000000
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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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Gapop 10.0 , Gapext 1.0
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1081
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em_htgo_hum: *
em_htgo_mus: *
em_htgo_other: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | ቴ ፋ ፋ ሀ ፋ የህ | C 42 | c 40 | 39 | 38 | ى د 7 0 | ıω | 34 | ω u | 32 | ט ני | 29 | 28 | 27 | 2 1 | 2 C | 23 | 22 | 21 | | c 19 | | 0 16 | | 14 | 13 | 5.5 | 10 | | m | -1 (| ט ת | 0 | | | | No | Regult | |
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| | 12.1 | o įo | 12.3 12.2 | | 12.4 | 12.5 | | • | 13.6 | 13.6 | 13.9 | 13.9 | 13.9 | 13.9 | 11. | 14.2 | 14.2 | 14.7 | ٠. | • | 22.4 | | ٠, | ٠ | ü | ωļ | 92.0 | | ۳ | Ψ | 96.8 | ۰. | 100.0 | • | 100.0 | 100.0 | Match | Ouery | æ |
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| ALIGNMENTS | AF348078 BC030948 | AC120742 | AF069555 AC116265 | AL590151 | G28604 | GDPZY3 | AF432354 | AF242850 | BTP2YRECP | BTIT34041 | AC013251 | AC021662 | HSA569 | HSU42030 | HC1142020 | AC124692 | MMU245636 | RNU22830. | MMU22829 | AF031897 | AX244775 | AX147814 | AC108794 | AX147840 | AX464561 | AX305130 | AB083598 | AX384211 | AX379468 | AX148186 | AF370886 | AC026756 | AL356486 | AX379470 | 339 | AX458238 | Ð | | SUMMARIES |
| | | Rattu | AF069555 Meleagris | AL590151 Zebrafish | = | X98283 G.domesticu | AF432354 Xenopus 1 | AF242850 Raja erin | X87628 B taurus | ACIUS/95 Rattus no | | | 45 Huma | 1142030 Human POVI | S81950 PZ purinoce | AC124692 Mus muscu | | U22830 Rattus norv | U22829 Mus musculu | AF031897 Meleagris | AX384210 Sequence | | | | | AX305130 Semience | Homo | Seque | • | | AF370886 Homo sani | 6756 | | 9470 Seque | 5877 | AX458238 Sequence | cription | | |

| TITLE | AUTHORS | REFERENCE | ORGANISM | SOURCE | KEYWORDS | VERSION | ACCESSION | DEFINITION | rocus | RESULT 1 AX458238 |
|--|---|--|--------------|--------|----------|------------------------|-----------|------------|---|----------------------|
| Rysek,R.P. A novel human g-protein coupled receptor, hgprbmy23, expressed | Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and | Mammalla, Butheria, Primates; Catarrhini; Hominidae; Homo. | Homo sapiens | human. | | AX458238.1 GI:21724972 | AX458238 | | AX458238 1081 bp DNA linear PAT 08-JUL-2002 | |

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BASE COUNT
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CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTACCCTTCCATATCTTGAGGGTCA
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                                                                                                                                                                                                                                                                 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA 660
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                                                                                       ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 780
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/protein_id="BAC06095_1"
/db_xref="GI:21929019"
/translation="MMEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIF
/translation="MMEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIF
LVGFPGNAVVISTYIFKMRPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFG
DFWCKFIRTSFHFNLYSSILFLTCFSITRYCVIIHPMSCPSIHKTRCAVVACAVVWII
SIVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKWYNLILTATTFCLFLVIVTLCY
TTIIHTLTHGLQTDSCLKQKARRITILLILLAFVCFLFFHILTVIRIESRLLSISCSI
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Matches 1081; Conserva
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                        GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
  GACCTTGGAAGAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
                                                                        TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGGTAGTATCCACTTACATTTTCAAAATGA 240
                                                                                                                          AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCTTTTGGAA
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Sequence 3 from Patent WO0187980
AX379470
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Mammalia; Eutheria;
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                                  Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 156555)

Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,

Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,

Federspiel,N., Glukhov,S., Hansen,N., Morehouse,A.J., Nguyen,M.
                                                                                                                                                                                     Homo sapiens chromosome 13 clone AC026756
             Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,Yu,S. and Davis,R.W.
Unpublished
                                                                                                                                                Homo sapiens.
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Best Local Similarity
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                                  GACCTTGGAAGAGCAGCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
                                                                GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTTGGCCTGCACAGATCTGCTGTATC
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                                                                                                                        TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA
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                                                                                                                                                TCTTCCTCGTGGGATTTCCAAGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA
                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
On Feb 23, 2001 this sequence version replaced gi:12745089
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Submitted (23-FEB-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Lam, B., Mao, J., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J., Yu, S. and Davis, R.W.
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------ Project Information
Center project name: 870
Center clone name: RP11-286P8
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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| 9 | CCCGAPTTATGCAGCTGCTTTTTGGAAATTGCATCAACAACAAATTATTCAACAACAACATTCTCATTCAACAA | |
| DЪ | 1 CCCGATTATGCAGCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCAC 12 | |
| Q | 6 TACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTTCCAGGCAATGCAGTAGTG 21 | |
| DЬ | 21 TACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTG 1 | |
| Ş | 16 ATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGAC | |
| DЬ | 1 ATATCCACTTACATATTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAAC | |
| Ş | CTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTT | |
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| Q | 336 AGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCAT 395 | |
| Дb | 10 | |
| Q | 6 TTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCT | |
| Db | 61 | |
| δ | 56 ATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTG | |
| 망 | 21 ATCATTCACCCAATGAGCTGCTTTTC | |
| Q | GCTGTGGTGTGGATCATT | |
| DБ | 81 GCTGTGGTGTGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCAC | |
| δ | 76 ACCAACAGGACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTY | |
| 뫄 | CCAACAGGACCAACAGA | |
| ঠ | 36 ATTAAGTGGTACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTG | |
| 뮰 | 01 ATTAAGTGGTACAACCTGATTTTGACTGCAACTA | |
| Ş | 96 ACACTTTGCTATACCACGATTATCCACACTCTGGACCCCATGGACTGCAAACTG | |
| рь | 1 ACACTITGCTATACCACGATTATCCA | |
| Ş | 756 CTTAAGCAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTTACGTATGTTTT 815 | |
| D | 721 CTTAAGCAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTT 780 | |
| Ş | 6 TTACCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGGCCTGCTTTCAATCAC | |
| υЬ | 81 | |
| Ş | 6 TCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATT | |
| В | 41 | |
| Q | 6 ACCITIGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCA | |
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| Ą | TCAACAGTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAG | |
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          Ramakrishnan,S.

Regulation of human p2y1-like g protein-coupled Patent: WO 0214511-A 5 21.FEB-2002;

Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Sequence 5
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAQATGGAAA 1013
                                                                                       AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                               CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTTGGTAACCTGTTA 953
                                                                                                                         AGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTTACCCTTTCCATATCTTG
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                                                           TCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAGCAGCAACAGGA
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Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada Location/Qualifiers
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/product="g protein-coupled receptor"
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/protein_id="AAL26480.1"
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/db xref="gi:16566323"
/translation="MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLFVIYGIIF
LVGFFGNAVVISTYLIKMRPWKSSTIINLNIACTDLLYLTSLEFFLHYYXASGENWIFG
DFMCKFIRESHFFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVVACAVVWAII
SLVAVIPMTFLITSTMRTNRSACLDLTSSDELAVIKWYNLILTATTFFCLFLVIVTLCY
TTIHTLTHGLQTDSCLKQKARRLTILLLLAFYVCFLFFHILRVIRIESRLLSISCSI
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              GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC
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                                                                        GTAAGCGGGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA 1067
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Patent: WO 0187937-A 10 22-NOV-2001;
Incyte Genomics, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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/note="Incyte ID No: 6575963CB1"
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                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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99.9%;
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Pred. No. 6.9e-253;
0; Mismatches 1;
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Database

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| 4 93.8 1014 24 ABN8530 Human 4 93.8 1014 24 ABK11381 Human 4 93.8 1014 24 AAK98323 Human 4 93.7 1014 24 AAG9847 4 93.7 1014 24 AAG9847 8 AAG9327 8 Human 9 3.7 1014 24 AAG9478 Human 9 3.7 1014 24 AAG9478 9 Human 9 3.7 1014 24 AAG947 9 Human 9 3.7 1010 22 AAH51011 9 3.5 1011 24 AAG947 9 Human 1 93.5 1011 24 AAG947 9 Human 1 93.5 1011 24 AAG947 9 Human 1 93.6 1012 22 AAK52430 9 Human 1 96.7 1020 22 AAK52430 9 Human 1 96.8 740 23 ABV15662 9 Human 1 97.1 1313 22 AAK52430 1 Human 1 97.1 1313 22 AAK52430 1 Human 1 97.1 1313 22 AAK52430 1 Human 2 55.8 740 23 ABV15662 9 Human 1 97.1 1313 22 AAK52430 1 Human 1 97.1 1313 22 AAK52430 1 Human 1 97.1 1313 22 AAK52430 1 Human 1 97.1 1313 22 AAK524310 1 Human 1 97.1 1313 22 AAK52310 1 Human 1 97.1 1313 22 AAK93310 1 Human 1 97.1 1313 22 AAK9310 1 Human 1 97.1 1313 22 AAK9310 1 Human 1 97.1 1313 22 AAK9310 1 Human | | | 23 | 442 | 31.3 | 338.2 | |
| 4 93.8 1014 24 ABN8530 Human 93.8 1014 24 ABK11381 Human 4 93.8 1014 24 AAK98323 Human 4 93.7 1014 24 AAK98323 Human 93.7 1014 24 AAD26370 Human 93.7 1014 24 AAD26370 Human 93.7 1014 24 AAD26370 Human 93.7 1010 22 AAH51011 93.5 1011 24 AAL43942 Human 1 93.5 1011 22 AAH51011 1 93.5 1011 22 AAH51011 1 93.5 1011 22 AAH51021 Human 1 76.9 831 22 AAH51011 1 76.9 831 22 AAH5102 1 1313 22 AAK52430 Human 1 72.1 1313 22 AAK52430 Human 1 73.8 548 23 ABV39127 Human 1 549 23 ABV39127 Human 1 540 23 ABV39127 Human 1 530 23 ABV39127 Human 1 531 24 ABC 23 ABV39130 Human 1 531 426 23 ABV39130 Human 1 531 426 23 ABV39130 Human 1 531 426 23 ABV39130 Human | | | 23 | 435 | 33.7 | 364.8 | |
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| 4 93.8 1014 24 ABN8530 Human 4 93.8 1014 24 ABK11381 Human 4 93.8 1014 24 AAK98323 Human 4 93.7 1014 24 AAK98323 Human 4 93.7 1014 24 AAD78847 8 AD78847 9 AD79847 9 AD79847 9 AD79847 9 AD79847 1 014 24 AAD34278 1 Human 9 AD79847 1 014 24 AAD3437 1 Human 9 AD79847 1 010 24 AAD3437 1 Human 1 93.5 1011 24 AAL3942 1 Human 1 93.5 1011 24 AAL3942 1 Human 1 93.5 1011 24 AAL3942 1 Human 1 93.6 1012 22 AAK5101 1 1313 22 AAK52430 1 Human 2 AAK52430 2 AAK52430 4 72.1 1313 22 AAK52430 2 AAK5393 4 44.4 545 22 AAK5391 8 44.4 545 22 AAK5341 8 Human 1 35.6 245 24 ABK11380 1 Human 1 H | | | 23 | 426 | 35.4 | 382.4 | |
| 4 93.8 1014 24 ABN85330 Human 93.8 1014 24 ABK11381 Human 4 93.8 1014 24 AAK98323 Human 4 93.7 1014 24 AAD34278 Human 93.7 1014 24 AAD34278 Human 93.7 1014 24 AAD34278 Human 93.7 1014 24 AAD26370 Human 93.7 1012 24 AAL43942 Human 93.7 1020 22 AAH51011 Human 1 93.5 1011 24 AAL52630 Human 1 93.5 1031 22 AAK52430 Human 1 76.9 831 22 AAK52430 Human 1 76.9 831 22 AAK52430 Human 4 72.1 1313 22 AAK52430 Human 4 72.1 1313 22 AAK52430 Human 4 93.8 578 22 AAH50998 Human 8 44.4 545 23 ABV39127 2 39.4 539 23 ABV45465 Human 5 35.6 2245 24 ABK11380 Human | Ξ. | | 23 | 478 | • | 384.4 | |
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| 014 93.8 1014 24 ABN85630 Human | | | 24 | 1014 | • | 1014 | |
| | _ | ABN8563 | 24 | 1014 | ٠ | 1014 | |

ALIGNMENTS

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Bruess M,
                                                                                                            22-SEP-2000; 2000DE-1046970.
                                                                                                                                                 22-SEP-2000; 2000DE-1046970.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; P2Y1-li; chromosome 13; G protein-coupled; receptor; gene therapy; thyroid; ds.
                                       (BRUE/) BRUESS M. (BOEN/) BOENISCH H.
Boenisch H;
                                                                                                                                                                                                                                                                                                                  3188..4201
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                           /product= "P2y1-like purine receptor"
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Result

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P-PSDB; AA014027.
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Novel isolated G-protein coupled receptor peptide useful for treating disorder characterised by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise antibodies

Claim 23; Fig 3; 64pp; English.

The present specifically claimed human genomic DNA sequence (located on CC chromosome 13) encodes a purinergic-related G-protein coupled receptor CC (GPCR) of the invention. GPCRs constitute a major class of proteins CC responsible for signal transduction within a cell. Upon binding of a CC ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The CC purinergic GPCRs (e.g. the P2Y receptors) - P2Y receptors are CC characterised by their selective responsiveness towards ATP and its CC analogues, some also respond to UTP. The invention comprises a human CC protein coupled receptor protein and encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein of the gpcreation for the development/identification of the arctivity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR nucleic acids of the invention are useful in diagnostic assays to controlling GPCR expression; and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals.

Sequence 9905 BP; 2656 A; 2218 C; 2061 G; 2970 T; 0 other;

B 맑 S 밁 Ś 밁 S В Ś 밁 밁 밁 8 Ś S Query Match 100.0%; Best Local Similarity 100.0%; Matches 1081; Conservative 0; 8496 8316 8256 CATATTGCCAAACTGAACTCTCTTGTTTTCTTGCAAGAGAAAGGAGACAACCATGAATG 8676 8616 8436 8376 301 241 481 CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGGTGTGGGTGTGGATCATTTCACTGG 540 121 61 μ TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT ATTICATGTGTAAGTTTATCCGCTTCAGCTTCCAGTTTCAACCTGTATAGCAGCATCCTCT GACCTTGGAAGAGCAGCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT 420 TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAAACTGGATCTTTGGAG TGACCAGCCTCCCCTTCCTGATTCACTACTATTGCCAGTGGCGAAAACTGGATCTTTGGAG 360 GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC 300 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTTACATTTTCAAAATGA 8495 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA 240 AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCTTTTGGAA 8375 AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCTTTTGGAA 120 CATATTGCCAAACTGAACTCTCTTGTTTTTCTTGCAAGATGAAAGGAGAGAACCATGAATG 60 Score 1081; DB 24; Pred. No. 1.9e-306; 0; Mismatches 0; Indels Length 9905; 0; Gaps 480 8675 8735 8615 8555 8315

| 5 | | Db 9 | Qy | Db 9 | Ş | Db s | ş | рb 9 | Ś | Db 9 | Ş | Db & | Ś | 망 | Ş | р 5 | Ş | Dp. | Q | 땅 |
|-------------|-----|--|---|--|---|--|---|--|---|--|--|--|--|--|---|--|---|---|---|--|
| 7330 C 7336 | ი—ი | 9276 GGAACCTTGAGCAAAGCAAAGAAATTAGTTACTCAAACCACCCTTGAAATATTTCATTTA 9335 | 1021 GGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAAACAACCCTTGAAATATTTCATTTA 1080 | 9216 TGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG 9275 | 961 TGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG 1020 | 9156 CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG 9215 | 901 CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTTGGTAACCTGTTACTATATG 960 | 9096 TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG 9155 | 841 TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTTCCATTGAGAATCAGATCCATGAAG 900 | 9036 CCATTCTGCTACTCCTTGCATTTTTACGTATGTTTTTACCCTTCCATATCTTGAGGGTCA 9095 | 781 CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTTTT | 8976 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 9035 | 721 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 780 | 8916 CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC 8975 | 661 CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTTGCTATACCACGATTATCC 720 | 8856 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA 8915 | 601 GTCTCGACCTACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA 660 | 8796 TAGCTGTCATTCCGATGACCTTCTTGATCACCATCAACCAAC | 541 TAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAAC | 8736 CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGGTGTGGTGGATCATTTCACTGG 8795 |

RESULT 3 AAS08362

0,

AAS08362 standard; cDNA; 1729 ВP

26-SEP-2001 (first entry)

Human cDNA encoding G-protein coupled receptor, GPCR 39404.

Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymp Heymann nephritis; Paget's disease; Crohn's disease; endometriosis; systemic lupus erythematosus; actinic keratosis; myocarditis; Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasm; inflammations; teratoma; ss. Homo sapiens. Human; G-protein coupled receptor; GPCR; 39404; immunogen; antibody;

Location/Qualifiers 294..1307 /*tag= a /product= "Protein 39404"

WO200149847-A2

12-JUL-2001.

22-DEC-2000; 2000WO-US35309.

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a nucleotide sequence given in Tables 1-9 (ABY00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
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(a) assessing whether a patient is affilicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
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(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient,
(h) assessing the aggressiveness or indolence of prostate cancer in a
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RESULT 7
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16-MAR-2000;
25-MAX-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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pharmacogenomic marker;
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gene; ss.
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The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) o

) comprising of the

Claim 1; Page 6487-6488;

11750pp; English

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -

WPI;

2001-662795/76.

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                                                                             CCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACA
                                                                                           CCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACA
                                                                                                                              TACCCTTCCATATCTTCAGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTT
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                                                                                                                                      Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
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26-SEP-2000;
26-SEP-2000;
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10-APR-2000;
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11-FEB-2000;
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23-DEC-1999
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17-NOV-1999
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2000US-0203630.

2000US-0210741.

2000US-0210992.

2000US-0226760.

2000US-0235418.

2000US-02354719.

2000US-0235473.
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99US-0171902.
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2000US-0196078.
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'product= "hRUP21"
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The sequence encodes a human G-protein coupled receptor (GPCR), hRUP21 The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists,

Claim 55;

Page 113-114; 159pp;

English

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GTAAGCGGGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA 1067
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                                       CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1013
                                                                        CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA
                                                                                        CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA
                                                                                                                                                                                     AGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTG
                                                                                                                        AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                                                      AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                                                                                        AGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTG
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Pred. No. 2.9e-287;
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05-JUN-2002
                             ABK11381;
                                                  ABK11381 standard; DNA; 1014
(first entry)
                                                    ВP
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Human DNA encoding P2Y1-like G protein-coupled receptor

Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR; infection; pain; cancer; anorexia; bullmia; asthma; hypotension; central nervous system disease; acute heart failure; hypertension; urinary retention; osteoporosis; diabetes; angina pectoris; myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis; benign prostatic hypertrophy; psychosis; neurological disorder; dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder; Tourette's syndrome. Parkinson's disease; anxiety; schizophrenia; manic depression; dementia; severe mental retardation; Huntington's disease;

sapiens

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WO200214511-A2
                            /*tag=
                                         Location/Qualifiers
                   /*tag= a
/product= "P2Y1-like
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21-FEB-2002.

10-AUG-2001; 2001WO-EP09243

14-AUG-2000; 2000US-224989P

(FARB) BAYER

Ramakrishnan

2002-257607/30.

Novel human P2Y1-like G protein-coupled receptor polypeptide which can be regulated for treating infection, pain, cancer, diabetes, anorexia, asthma, hypertension, neurological disorder and dyskinesia can

Claim 1; Fig 5; 118pp; English.

CC receptor (GPCR) polypeptide and the nucleic acids encounty in (including 5 and 3 sequences, promoters, fragments, variants, or a CC sequence encoding a protein at least 50% identical to the GPCR). CC Also included are an expression vector comprising the nucleic acid, a host cell containing the vector and the identification of modulators of the GPCR especially those that reduce the activity of the GPCR. CC The nucleic acid is useful for detecting a polynucleotide encoding the GPCR in a biological sample. The GPCR and nucleic acid are useful for for modulators of the GPCR. The modulator or agent useful for modulators of the GPCR. The modulator or agent useful for modulators of the GPCR. The modulator or agent useful for modulators of the GPCR. The modulator or agent useful for modulating cc the activity of P2Y1-like G protein-coupled receptor in a disease such as anorexia, bulimia, asthma, central nervous system (CNS) disease, acute heart failure, hypotension, hypertension, urinary retention, cancer, osteoporosis, diabettes, angina pectoris, mycardial infarction, ulcer, osteoporosis, diabettes, angina pectoris, benign prostatic hypertrophy, cc psychotic and neurological disorders, dyskinesias, HIV virus infection of Alsease, anxiety, schizophrenia, manic depression, delirium, dementia, ABKIL1381

AD AB The invention relates to a purified human P2Y1-like G protein-coupled receptor (GPCR) polypeptide and the nucleic acids encoding it

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GTAAGCGGGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA
                               CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA
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                                                                           CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA
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Pred. No. 2.9e-287;
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RESULT 13
ABG778847
ID ABG778
XX Human
XX EP121
XX EP122
XX 04-OCT-2002 ABQ78847; ABQ78847 standard; cDNA; (first entry) 1014 BP

Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective; anti-inflammatory; cytostatic; cardiovascular; antiallergic; hypotensive; antiarteriosclerotic; osteopathic; hypertension; asthma; artherosclerosis; gene; ss. Human G-protein coupled receptor PFI-019 CDNA

EP1219638-A2 sapiens. /*tag= a /product= Location/Qualifiers /*tag= "PFI-019"

18-DEC-2000; 2000GB-0030854. 04-MAY-2001; 2001GB-0011031. Fidock MD; 04-DEC-2001; (PFIZ) 03-JUL-2002. PFIZER LTD. PFIZER INC. 2001EP-0310136

New G-protein coupled receptor (GPCR) polypeptide with homology to P2Y purinoreceptor, useful for treating e.g. inflammation or cancers in a patient, or for screening GPCR agonists or antagonists for treating diseases

WPI; 2002-521945/56. P-PSDB; ABB81902.

Claim 1; Page 12; 19pp; English

The invention relates to a novel G-protein coupled receptor (GPCR), and the polynucleotide encoding it. The protein of the invention has neuroprotective, anti-inflammatory, cytostatic, cardiovascular, antiallergic, hypotensive, antiarteriosclerotic, and osteopathic activity. The GPCR polypeptide is useful for manufacturing a medicament for treating a patient who needs to upregulate a receptor. Preferably, therapeutically useful areas are hypertension, asthma, and artherosclerosis. The sequence encodes the G-protein coupled receptor of the invention, pFI-019.

Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Sub-N.C

밁 Ś 묽 S Query Match 93. Best Local Similarity 99. Matches 1013; Conservative 114 61 54 ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCT 1.3 93.7%; 0, Score 1012.4; DB 2 Pred. No. 8.5e-287; 0; Mismatches 1; DB 24; Indels Length 1014; .: Gaps 60 0

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                GTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCACCCTTGA 1067
                                             CTATATGTGGTGATCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA
                                                         CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA
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RESULT 15
AAD26370
ID AAD26
XX AAD26
XC AAD26
XX AAD26
XX Humar
XX Arte:
XW Aflzhr
XW Addi
atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder; acquired immune deficiency syndrome; inflammatory disorder; infection; addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
                                                                                                     Human; G-protein coupled receptor 2; cell proliferative disorder; arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
                                                                                                                                                                                                                           Human G-protein coupled receptor 2
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18-MAY-2000;
22-MAY-2000;
25-MAY-2000;
02-JUN-2000;
02-JUN-2000;
                                                                                                                                                                                                                                      The invention relates to human G-protein coupled receptor (GCREC) polypeptides and polynucleotides. GCREC polypeptides are useful for screening compounds that modulate their activity. They are useful in the diagnosis, prevention and treatment of disorders which include cell proliferative disorders such as arteriosclerosis, hepatitis, myelofibrosis, psoriasis and cancer including adenocarcinoma, leuka
                                                                                                                                                                                                                    lymphoma; neurological disorders such as epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease,
                                                                                                                                                                                                                                                                                                                                          Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
                                                                                                                                                                                                                                                                                                                  Claim 5;
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Khan FA, Gandhi
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DB; AAE16171.
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; 2000US-208834P.
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CP Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral cardiovascular disorders such as arteriorenous fistula, atherosclerosis, bacterial and viral convertension, vascular tumours, myocardial infarction, hypertension, vascular tumours, myocardial infarction, hypertensive convertension acquired infarction, hypertensive constribution, acquired immune deficiency syndrome (Alis), diarrhoea, constipation, acquired immune deficiency syndrome (Alis), hapatic constipation, acquired immune deficiency syndrome (Alis), hapatic conscipatiopathy; autoimmune/inflammatory disorders such as Addison's conscipatitis, crohn's disease, diabetes mellitus, Goodpasture's syndrome, contact dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, contact dermatitis, systemic lupus exythematosus, uveitis, viral, bacterial, contact fungal, parasitic, protozoal and helminthic infections and trauma; contact contact disorders such as diabetes, obesity and osteoporosis; and contact contact disorders such as infection caused by viral agent classified as contact as useful as grobes for assessing toxicity of test compounds. They are coupled receptor 2 (GCREC-2) cDNA. dementia, leukaemia,

Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other

Query Match
Best Local Similarity
Matches 1013; Conser 93.7**%**; Score 1012.4; Pred. No. 8.5e 0; Mismatches <u>,</u> 8.5e-287; DB 24; Length 0, Gaps

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Minimum DB
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Sequence:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| ტ | _ر | 4 | ω | 2 | — | Result No. |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-----------------------------|
| 108.8 | 109.4 | 114.6 | 115.6 | 126.6 | 257 | Score |
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| 663 | 877 | 638 | 641 | 623 | 744 | ength I |
| 13 | 12 | 9 | 14 | 14 | 14 | ∺ |
| BM426517 | BG402029 | AL675845 | BQ396255 | BQ038875 | BM723768 . | DB ID |
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Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

| 4 | 4 1 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | Ç | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | φ | æ | 7 |
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| • | 86.8 | . 6 | 7. | • | • | • | • | • | • | • | • | • | • | | | 92.6 | • | 93.6 | 93.8 | 93.8 | • | 94 | 94 | 94 | 94 | 95.8 | S | 96 | 97.2 | 98.4 | 99.6 | 100 | 100.4 | 100.4 | 102 | 103 | 106.2 | 107.4 |
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| 1101 | 869 | 570 | 585 | 529 | 2146 | 1057 | 885 | 870 | 801 | 752 | 734 | 581 | 589 | 678 | 899 | 983 | 934 | 955 | 839 | 523 | 484 | 936 | 898 | 884 | 420 | 1063 | 408 | 639 | 851 | 606 | 801 | 422 | 3001 | 2542 | 520 | 609 | 491 | 1101 |
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| CNS 04 VV3 | BQ724793 | BG579061 | BE627479 | AA177828 | BC027965 | BM918711 | AL546894 | AL545172 | BI837965 | BM008116 | BG914321 | BM258063 | BQ396804 | BE314834 | BQ959110 | CNS045P5 | BI768397 | AL521440 | BQ897419 | AL836006 | BQ551383 | AL520218 | BI819396 | AL525099 | BB864882 | BM918491 | BI401676 | BB660768 | BI833118 | AZ953874 | BG924078 | BB847918 | AK005013 | AK017378 | AI663305 | AL588350 | BG712193 | CNS05328 |
| . AL309576 Tetraodon | 24793 AGENCOUR | df22e05. | w | mt 07f | | 1 AGENCO | AL546894 AL546894 | AL545172 AL545172 | BI837965 603083801 · | BM008116 603618002 | BG914321 602810633 | BM258063 522739 MA | z | BE314834 601147561 | | Tetraodo | J | | ø | ъ | w | L520218 | o. | ٠. | BB864882 BB864882 | | | | BI833118 603090834 | AZ953874 2M0219L17 | BG924078 602823635 | | | œ | | | 12193 | AL318925 Tetraodon |

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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM RESULT 1 BM723768 LOCUS VERSION KEYWORDS COMMENT ACCESSION DEFINITION JOURNAL MEDLINE BM723768 BM723768.1 BM723768 744 bp mRNA linear EST 01 UI-E-E01-aix-g-16-0-UI.rl UI-E-E01 Homo sapiens cDNA clone UI-E-E01-aix-g-16-0-UI 5', mRNA sequence. 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Contact: Soares, MB
Program for Rat Gene
University of Iowa discovery 1 (bases 1 to Bonaldo, M.F., Email: msoares@blue.weeg.uiowa.edu Normalization and subtraction: two approaches to facilitate gene Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens 97044477 Genome Res. 6 (9), 1 to 744) GI:19045099 Lennon, G. and Soares, M.B. 791-806 (1996) Discovery and Mapping EST 01-MAR-2002

KEYWORDS

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TTGTTACCACCAGTTCCAATGGGGACAGCACCACCTGCCATGACACTTCCAGCGTGGATC
                                    TGATCACATCAACCAACAGGACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg,
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1 (bases 1 to 641)
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/dev_stage="embryo, stages 14-19"
/lab_host="DHIOB (phage-resistant)"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: NotI; Site_2:
EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average
insert size 2.1 kb. Constructed by Invitrogen. Note: This
is a Xenopus Gene Collection (XGC) library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
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Email: trop@eanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus tropicalis EST project 2001
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Sanger Xenopus tropicalis
Unpublished (2001)
Contact: Taylor R
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Location/Qualifiers
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/lab host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNĀ from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
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/clone="TGas051n19"
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Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fishe Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysusing Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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Tetraodon nigroviridis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygii; Neoteleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Characterization and repeat analysis of the compact gen treshwater pufferish Tetraodon nigroviridis
                                                                                                                                                                              This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.ons.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTACGTGGGCATCTGCCACCCGATTAAGGCGCTGAATCTGGTGAANCCCCCGANATTCCT 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 bp mRNA linear EST 08-MAY-2001 pglln.pk011.f3 Normalized Liver Library Gallus gallus cDNA clone pglln.pk011.f3 5' similar to gbl AAC60339.1 (AF031897) G protein coupled P2Y nucleotide receptor [Meleagris gallopavo]G, mRNA
                                                                                                                                                                                                                                                             Burnside, J., Morgan, R.W. and Co
Chicken ESTs from a normalized
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani Phasianinae; Gallus.
                                                                                                                                                                 Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                              Molecular Endocrinology University of Delaware
                                                                                                                                                                                                                                                 Contact: Joan Burnside
                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                  chicken.
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58; Conservative
                                                                                                                                                                                                                                                                                                              (bases 1 to 491)
                                                                                                                               joan@UDel.Edu, www.chickest.udel.edu
Location/Qualifiers
                               /clone_lib="Normalized Liver
/sex="Male and Female"
                                                                                  organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                   1. .491
                                                            clone="pglin.pk011.f3"
'tissue_type="liver"
'lab_host="E.coli EM
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Pred. No. 1.3e-19;
0; Mismatches 216;
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alized liver library
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                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490 TAGTGACCTTAGAAGTTCTACCCATG 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCACTGGTAGCTGTCATTCCGATG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATGCTCTTGCTCACTGTCATTATCATGGACCGATATCTGCTCATGAAGTACCCTGTCC
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                          Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                        Z54Z bp mRNA linear HTC 19-JAN-200 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430432J15:purinergic receptor P2Y, G-protein coupled 2, full insert sequence.

AK017378
                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                            AK017378.1 GI:12856588
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                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                           Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shot be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for
                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                      Metazoa;
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                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 3.4e-18;
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                                                                                                                                                                                                                               Sciurognathi;
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                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URLihttp://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
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    Division of Experimental Animal Research
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/gene="P2ry2"
/note="putative"
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VLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVDFSVILVCY
VLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHLTRTLYYSFRSLDL
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VLGLCLNVVALYIFLCRLKTWNASTIYMFHLAVSDSLYAASLPLLVYYYARGDHWPFS
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/db_xref="MGD:MGT:1895057"
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                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
Email: genome-res@gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
                                                                                                                                                                                                                                   Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9B847918 RIKEN full-length enriched, adult male clone F530201F11 5', mRNA sequence.
                                                                                              1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                           Fax: 81-45-503-9216
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                                                                                                                Yokohama, Kanagawa 230-0045, Japan
  Sugahara, Y.,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes; R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0219 row: L column: 1
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606 bp DNA linear GSS 27-APR-200
2M0219I17F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0219I17 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gli4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XiIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical
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/strain="C57BL/6J"

/db_xref="taxon:10090"
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ote="Vector: PWD42nv; Purified genomic DNA from M.
sculus C57BL/6J (female) was obtained from the Jackson
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GCTGCCACATGCATCCATCGCAACCGCACTGTGTGCTACGACCTGAGC 507
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                                                                  GTAGCCTGTGCTGTGGTGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTG
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Search completed: January 30, 2003, 11:05:45 Job time: 2204 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2 6/ptodata/1/ina/5B_COMB.seq:*
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US-08-513-9748-57
US-08-513-9748-37
US-08-513-9748-37
US-08-486-6738-62
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108 GCTGCTTTTGGAAAATGCACTGAAGAAGATGCACTACCTCCCTGTT 167
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| Query Match 11.9%; Score 129; DB 2; Length 1 Best Local Similarity 50.1%; Pred. No. 1.4e-29; Matches 380; Conservative 0; Mismatches 370; Indels | SCHIT 1 S-08-559-524A-1 S-08-559-524A Sequence 1, Application US/08559524A Patent No. 5871963 GENERAL INFORMATION: APPLICANT: Conley, Pamela B. APPLICANTON NOWEL PURINERGIC RECEPTOR NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEB: MORGAN, LEWIS & BOCKIUS LLP STREET: 1800 M Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20036-5869 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: NUMBER: OSS SOFTWARE: PATECHION DATA: MEDIUM TYPE: Ploppy disk COMPUTER: SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATECHION DATA: APPLICATION NUMBER: US/08/559,524A TILING DATE: 15-NOV-1995 CLASSIFICATION NUMBER: 03/988 REFERENCE/DOCKET NUMBER: 03/988 REFERENCE/DOCKET NUMBER: 0444481-5010-0-US TELEPHONE: 202-467-7100 TELEPHONE: 202-467-7176 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1996 base pairs TYPE: nucleic acid STRANDENESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA PEATURE: NAME/KEY: CDS LOCATION: 6251626 | ALIGNMENTS | 28 90.8 8.4 2453 5 PCT-US95-07180-1 29 87.2 8.1 1224 2 US-08-742-440A-1 30 84 7.8 1317 1 US-08-153-848-45 31 84 7.8 1317 3 US-09-299-843A-45 32 84 7.8 1317 4 US-09-288-3378-45 33 84 7.8 1317 5 PCT-US93-11153-45 34 84 7.8 1664 4 US-09-582-224A-5 35 84 7.8 1679 4 US-09-582-224A-5 36 84 7.8 1737 1 US-08-202-056-4 37 84 7.8 1737 1 US-08-076-093A-3 38 84 7.8 1737 1 US-08-076-093A-3 39 84 7.8 1737 2 US-08-265-3 40 84 7.8 1737 2 US-08-265-3 41 84 7.8 1737 2 US-08-802-627A-3 42 84 7.8 1737 2 US-08-802-627A-3 43 84 7.8 1737 2 US-08-801-238-3 44 84 7.8 1737 3 US-08-801-228-3 45 84 7.8 1737 3 US-08-801-228-3 46 7.8 1737 3 US-08-801-228-3 47 84 7.8 1737 3 US-08-08-262-63-3 48 7.8 1737 3 US-08-01-228-3 49 84 7.8 1737 3 US-08-01-228-3 40 84 7.8 1737 3 US-08-01-228-3 41 84 7.8 1737 3 US-08-01-228-3 |
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| 996; | | | Sequence |
| Gaps 2 | | | 1, Appli 1, Appli 45, Appl 45, Appl 45, Appl 45, Appli 5, Appli 14, Appli 14, Appli 13, Appli 3, Appli |

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US-08-442-134A-1
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Best Local Similarity
Matches 222; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
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NAME/KEY:
LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      282
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                          219 TCCACTTACATTTTCAAAATGAGACCTTGGAAGGAGCAGCACCATTATGCTGAACCTG 278
                                                                                                                         159 CTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATA 218
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/OFFILING DATE: 16-MAY-1995
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GCTGTGTCTGÄTGCACTGTATGCGGCCTCCCTGCCGCTGCTGGTCTÄTTACTÄCGCCCGC 341
                           GCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGT 338
                                                               TACATCTTCTTGTGCCGCCTCAAGACCTGGAATGCGTCCACCACATATATGTTCCACCTG
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No. 5596088th Carolina
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USA
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Post Office Drawer 34009
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57..1181
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Harden, Thomas K.
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Pred. No. 1.1e-21;
0; Mismatches 198;
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RESULT 4
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                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                            FEATURE:
                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                           FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
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LOCATION:
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                                                                                    LENGTH: 1842 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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STREET: Post Office Drawer 34009
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No. 5607836th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: Null Cells Expressing P2U Receptors
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INVENTION: DNA Enc
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Parr, Claude E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0,
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57..1181
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                                                                                                                                                                                                                                                                                                                            US 08/442,134
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Query Match Best Local Similarity

9.5%;

Score 103.2; DB 1; Pred. No. 1.1e-21;

Length 1842;

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496 GCTGCCACAGGCATCCAGCGCAACCGCACTGTGTGCTACGACCTGAGC 543

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Best Local Similarity
Matches 200; Conserv
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PRIOR APPLICATION NUMBER: JP 6-
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TELEPHONE: 617-523-3400
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567 ATCACATCAACCAACAGGACCAACAGATCAGCCTGTCTCGACCTCACC 614
                                                                                 507
                                                                                                             376 CTGGGCATCTGCCACCCCTGGCTTCCTGGCACAAGCGTGGAGGTCGCCGTGCTGCTTGG 435
                                                                                                                                                                                           316
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                450 TGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTT--- 506
                                                                                                                                                                                                                               390
                                                                                                                                                                                                                                                            256 TACGCCAGAGGGGACCACTGGCCCTTCGGAGACCTCGCCTGCCGCTTTGTACGCTTCCTC 315
                                                                                                                                                                                                                                                                                            330 TATGCCAGTGCCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGC 389
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                                     GTAGCCTGTGCTGTGGTGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTG 566
                                                                                                                                                                                  TTCTATGCCAATCTACATGGCAGCATCCTGTTCCTCACCTGCATTAGCTTCCAGCGCTAC 375
                                                                                                                                                                                                                       TTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTAC 449
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RESULT 7
US-08-513-974B-370
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Patent No. 611
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6.
FILING DATE: 30-SEP-1994
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
                                                                                                                                                  FILING DATE: 11-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-AUG-
                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 7.
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 7.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN ITLE OF INVENTION: PRODUCTION, AND USE THEREOF
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                                   NAME: Resnick, David S. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 7-007177
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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FILING DATE: 14-SEP-1995
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Ohgi, Kazuhiro
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Ohtaki, Tetsuya
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                                                                                                                                                                                           Sequence 1, Application US/08472840 Patent No. 5763575
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Best Local Similarity
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                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1475 base pair
                                  NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                              APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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APPLICATION NUMBER: US 08/390,301
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ADDRESSEE: MORRISUN & FULL STREET: 2000 Pennsylvania Ave. N.W.,
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                           GTTGTAGCCTGTGCTGTGTGGTGGTAGCTGTC 548
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ilarity 52.6%;
Conservative 0
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Pred. No. 4.3e-20;
0; Mismatches 192;
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                   Ste. 5500
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Best Local Sim.
Matches 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
FEATURE:
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LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
     802
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                                            504
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TELEFAX: 90-4030
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LOCATION:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
GGCGTCTCCTTGGCAATCTGGCTCCTGATTTTTTCTGGTCACCATC 846
                                       GTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACTGGTAGCTGTC 548
                                                                                                      CGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCA
                                                                                                                                        GGCTTTTTCTATGGTAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAG
                                                                                                                                                               TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTC
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                                                                      AGGTACTGGGTGATCGTGAACCCCCATGGGACACCCCCAGGAAGAAGGCCAAACATCGCCGTT
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Similarity 52.6%;
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.3e-20;
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RESULT 11 US-08-476-976-1

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US-08-486-673B-1
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Best Local Similarity 52.1
Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/097,938
PRIOR FILING DATE: 1993-07-26
PRIOR APPLICATION NUMBER: PCT/US94/08536
PRIOR FILING DATE: 1994-07-26
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Scarborough, Robert M.

TITLE OF INVENTION: Nucleic Acids Encoding the C140 Receptor FILE REFERENCE: 44481-5006-08-US CURRENT APPLICATION NUMBER: US/08/486,673B

CURRENT FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sundelin, Johan
APPLICANT: Scarborough, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THATION: (232)...(1416)
COCATION: (232)...(1416)
OTHER INFORMATION: C140 receivements information: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
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           444
                                       682 GGCTTTTTCTATGGTAACATGTATTGCTCCATCCTTCATGACCTGCCTCAGCGTGCAG 741
                                                                                              384
                                                                                                                                        622
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                                                                                 TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTC 443
                                                                                                                               TCCTACCACCTACATGGCAACAACTGGGTCTACGGGGAGGCCCCTGTGCAAGGTGCTCATT 681
CGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCA 503
                                                                                                                                                                                                                                                                                                   AATGGCATGGCCCTCTGGATCTTCCCTTTTCCGAACGAAGAAGAAGAACACCCCGCCGTGATT 561
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Pred. No. 4.3e-20;
0; Mismatches 192;
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US-08-476-000-60
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                                                                                                                                                                                                                                             Matches 213;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
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APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCO
324 CACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGC 383
                                         415
                                                                                                                                                                                                     144 CTCAAGATGCACTACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGC 203
                                                                                                                                204 AATGCAGTAGTGATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCAGCACCATC 263
                                                               264 ATTATIGOTGAACCTIGGOCTIGCACACATOTICCTIGTATICTIGACCAGOOTICCOOTTIGOTIGATIT 323
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CTTY: Washington
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STRANDEDNESS:
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5716789
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                                                                                                                                                                                                                                        Score 97.8; DE Pred. No. 6e-200; Mismatches
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                                  CTGTCATCTGGTTCCCCCTGAAGATC
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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1081
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(cgn2_6/ptodata/1/pubpna/US07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pubpna/US07_NEW FUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW FUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW FUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW FUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW FUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW FUB.seq:*
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cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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2051
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1689
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 US-09-828-478-1
US-09-826-291-5
US-09-866-230-6
US-09-828-478-3
US-09-828-478-3
US-09-728-952-26
US-09-788-133-1
US-09-880-107-2143
US-09-104-063-3
US-09-962-832-218
US-09-964-8248-100
                                                                                                                                                                                                                                US-09-943-798-3

US-09-943-798-1

US-09-728-422-1

US-09-812-102-40

US-09-826-791-1
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Sequence 2, Appli
Sequence 15, Appl
Sequence 100, App
Sequence 3, Appli
                                                          Sequence 3, Appli
sequence 1, Appli
sequence 40, Appl
sequence 1, Appli
sequence 1, Appli
sequence 1, Appli
sequence 5, Appli
sequence 3, Appli
sequence 26, Appli
sequence 21, Appli
sequence 21, Appli
sequence 2143, App
Sequence 218, App
Sequence 218, App
Sequence 20, Appli
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| | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|------------|-----------------|-----------------|------------------|------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|------------------|-------------------|------------------|-------------------|-------------------|-----------------|------------------|------------------|-----------------|------------------|-----------------|-------------------|-----------------|-------------------|
| | 69.6 | 69.6 | 69.6 | 69.8 | 69.8 | 69.8 | 69.8 | 70.6 | 71.4 | 71.8 | 72.4 | 72.4 | 72.4 | 72.4 | 73.2 | 73.4 | 73.4 | 73.4 | 73.8 | 74 | 77.2 | 81.6 | 82.4 | 82.4 | 82.4 | 82.6 |
| | 6.4 | 6.4 | 6.4 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.6 | 6.6 | 6.7 | 6.7 | 6.7 | 6.7 | 6.8 | 6.8 | 6.8 | 6.8 | 6.8 | 6.8 | 7.1 | 7.5 | 7.6 | 7.6 | 7.6 | 7.6 |
| | 1464 | 1464 | 1014 | 2632 | 2632 | 2268 | 1080 | 1083 | 1563 | 1892 | 1414 | 993 | 993 | 823 | 1860 | 2081 | 2080 | 1910 | 1083 | 1895 | 1083 | 2050 | 1955 | 1102 | 1080 | 3426 |
| | 9 | 9 | - | | | 10 | 9 | 10 | 5 | 9 | 9 | 10 | 10 | 12 | 9 | 12 | 12 | 10 | 5 | 9 | 10 | ø | 9 | 9 | 10 | 9 |
| ALIGNMENTS | US-10-166-113-1 | US-10-166-359-1 | US-09-791-932-55 | US-09-867-915-26 | US-09-867-915-1 | US-09-880-107-3034 | US-09-867-915-2 | US-09-852-156-9 | US-09-880-107-1611 | US-09-900-699A-1 | US-10-098-841-312 | US-09-954-456-1129 | US-09-826-508-15 | US-10-044-090-598 | US-09-940-240-17 | US-10-044-090-627 | US-10-044-090-628 | US-09-944-807-1 | US-09-852-156-11 | US-09-940-240-19 | US-09-852-156-7 | US-09-940-240-15 | US-10-190-469-2 | US-09-870-759-143 | US-09-739-151-1 | US-10-001-835-29 |
| | 1, | 1 | 55, | 26 | Sequence 1, Appli | | Sequence 2, Appli | Sequence 9, Appli | | Sequence 1, Appli | Sequence 312, App | Sequence 1129, Ap | 15, | Sequence 598, App | | 62 | 62 | 1, A | 11, | • | 97, | 15 | 2 | Sequence 143, App | e 1, | Sequence 29, Appl |

T GINETA

RESULT 1 US-09-943-798-3

Sequence 3, Application US/0943798
PATENT NO. US2002005215A1
GENERRAL INFORMATION:
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Polypeptide
FILE REFERENCE: QG1021
CURRENT APPLICATION NUMBER: US/09/943,798
CURRENT FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1014

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; ORGANISM: Homo sapiens
US-09-943-798-3
                                                                                                                                                                                                                                                               Best Local Similarity 100.0%; Matches 1014; Conservative 0
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Best Local Similarity
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                CTGTATCTGACCAGCCTCCCCTTCCTGATTCACTATGCCAGTGGCGAAAACTGGATC 353
                                                                   AAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTG
                                                                                                    GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC
                                                                                                                             GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC
                                                                                                                                                      ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCT 60
                                                                                                                                                                                                                                                            93.8%; Score 1014; DB 10;
100.0%; Pred. No. 9.2e-291;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/728,422
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 1
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Matches 792
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LOCATION: (547)..(1239)
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GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA
                                                                                                                                                 CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGGTGTGGATCATTTCACTGG
                                                                                                                                                                                                                                  TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT
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                                                                                                                                                                                                                                                                                   ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
                                                                                                                                                                                                                                                                                                                         TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG
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FILE REFERENCE: 5800-41 035000/183478
CURRENT APPLICATION NUMBER: US/09/812,102
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/812,102

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APPLICANT: Robison, Keith
TITLE OF INVENTION: No. US
FILE REFERENCE: 5800-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 515; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                        CTCCTTGCATTTTACGTATGTTTTTTACCCTTCCA
                                                                                                            CATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAACCATT
                                                                                                                                                                                                                                                                                   TTCTGCCTCCCCTTGGTGATAGTGACACTTTTGCTATACCACGATTATCCACACTCTGACC
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                                                                                                                                                                       CATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAACCATTCTGCTA
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RESULT 5
US-09-826-791-1
; Sequence 1, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:

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; NAME/KEY: CDS
; LOCATION: (1)..(1041)
US-09-866-230-6
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Patent No. US20020150901A1
GRMERAL INFORMATION:
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
PILLE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
DEBTOR AND TOWN NUMBER: 2001-05-25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
                             505 TTGTAGCCTGTGCTGTGGATCATTTCACTGG 540
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GGATCCTCTGTGGGATCATATGGATCCTTATCATGG 502
                                                                                         GCTACTGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAG 504
                                                                                                                           ATTCCTTGTÄTGTCÄÄCÄTGTÄCÄGCÄGTÄTTTATTTCCTGÄCCGTGCTGÄGTGTTGTGC
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                                                               GTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCT
                                                                                                                                                                                       ACTATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTT
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RESULT 10
US-09-728-952-26
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-828-478-3
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US-09-828-478-3
Sequence 26, Application US/09728952
Patent No. US20020111302A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09828478 Patent No. US20020155528A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: Regulation of Human CysLT2-Like
TITLE OF INVENTION: Protein
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Local Similarity 52.3%;
nes 207; Conservarium
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                                                                                                                                                                                                        GTTTCCTGGCAATGGTTCACCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCT 718
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Pred. No. 1e-17;
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CANT: Ujwal, Manusha L CANT: Drmanac, Radoje ' OF INVENTION: No. US2

Radoje T. No. US20020111302A1el Nucleic Acids Wang, Dunrui Yamazakı, Vicki

Liu, Chenghua Asundi, Vinod Wang, Jian-Rui

Tang, Y. Tom Zhou, Ping Goodrich, Ryle

INFORMATION:

US-09-880-107-2143

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RESULT 13
US-09-104-063-3
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Matches 244; Conserv
                                                                                   SOFTWARE: WinPatin (Gen-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 24-June-19:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, James
APPLICANT: Wood, WIlliam I.
TITLE OF INVENTION: PP4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   PRIOR APPLICATION DATA:
                 PILING DATE: 22-AUG-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602
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     APPLICATION NUMBER:
                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                            STREET:
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49.8%;
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08/664228
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Pred. No. 8e-15;
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Best Local Similarity 49.8%;
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NAME: LOVE, RICHARD D.

REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19-DEC-
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              354 CATCACGCTTCCCCTTCTGGGCAGT----TGATGCCGTGGCAAACTGGTACTTTGGGAA
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STRANDEDNESS: Single
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TELEX: 910/371-7168
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                                                                                                  TCTCGACCTC 611
                                                                                                                                                            CATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGGTGGGATCATTTCACTGGT
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Sequence 218, Application US/09962832
Patent No. US20020110821A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sig

FILE REFERENCE:

689290-74

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compugen Ltd.
/cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
/cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US07_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_COMB.seq:*
/cgn2_6/ptodata/1/pna/US09_COMB.seq:*
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    /cgm2_6/ptodat
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Match

Length BB

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1068 1068 1079.4 1079.4 1079.4 1079.4 1079.4 1079.4 1079.4 US-09-634-656-3 US-10-23-634-5 US-10-23-634-5 US-09-475-790-2 US-09-785-276A-24015 US-09-785-276A-29927 US-09-785-276A-30042 US-09-785-276A-30042 US-60-205-423-233 US-60-205-423-235 US-60-205-423-236 US-60-205-423-239 US-10-010-568-1 US-60-251-926-1 US-60-269-795-1 Description Sequence 1, Appli 1, Appli 1, Appli 2, Appli 3, Appli 3, Appli 4, Appli 4,

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; LENGTH: 1081
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(1067)
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                                                                                                                                                                              GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA
                                                                                                                                                                                                                                            TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA
TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
                                                CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA
                                                                                               ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA
                                                                                                                                              CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
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                                                                                                                                CTGCAACTACTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
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Sequence 1, Application US/60269795
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COL
TITLE OF INVENTION: KIDNEY
FILE REFERENCE: D0077 PSP 1
CURRENT APPLICATION NUMBER: US/60/269,795
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
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LENGTH: 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: homo |
FEATURE:
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LOCATION: (54)..(1064)
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TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATCACCCAATGAGCTGCTTTT
                                                             ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCAGTTTCAACCTGTATAGCAGCATCCTCT 420
                                                                                                                       TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG
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NUMBER OF SEQ ID NOS: 132
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO S: 150
LENGTH: 1560
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-634-5
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APPLICANT: Millet, Isabelle
APPLICANT: Gerlach, Valerie
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-221
CURRENT APPLICATION NUMBER: US/10/023,634
CURRENT PILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,025
PRIOR APPLICATION NUMBER: 60/265,163
PRIOR APPLICATION NUMBER: 60/265,163
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/272,929
PRIOR APPLICATION NUMBER: 60/272,929
PRIOR APPLICATION NUMBER: 60/274,864
PRIOR APPLICATION NUMBER: 60/274,864
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
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Best Local Similarity 99.9
Matches 1080; Conservative
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PRIOR FILING DATE: 2001-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-07-31
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APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
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APPLICATION NUMBER: 60/277,880
FILING DATE: 2001-03-22
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                                                      AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCTTTTGGAA 419
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Edinger, Shlomit R
Gangolli, Esha A
Malyankar, Uriel M
Gunther, Erik
Smithson, Glennda
Millet, Imabelle
Gerlach, Valerie
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Gusev, Vladimir Y
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Tchernev, Velizar T
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Zerhusen, Bryan D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-04-25
                                                                                                                                                                                                                                             99.9%; Score 1079.4; DB 38; Length 1560; 99.9%; Pred. No. 5.9e-299; tive 0; Mismatches 1; Indels 0;
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                                                                    RESULT 6
US-09-475-790-2
Sequence 2, Application US/09475790 GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
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| 8 | 420 181 480 241 540 301 600 361 660 421 720 720 541 840 661 900 661 900 661 | |
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| 음 성 음 | 660 421 720 | ATTICATOTOTANGTITATICCGCTTCAGCTTCCATTCAACCTGTATAGCAGCARC TCCTCACCTGTTTCAGCTCCTCCGCTACTGTGTGAGCACATCAATCA |
| 유 성 | 481 780 | CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACAATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACA |
| 음 성 | 541 840 | TAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCGACAGGACCAACAGATCA |
| 음 성 | 900 | GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATT? |
| 8 8 | 960 | CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTTGCTATACCACGATTP |
| 음 성 | 721 1020 | ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGG |
| ß 8 | 781 1080 | CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGG |
| 용 성 | 841 1140 | TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATG |
| 용 성 | 901 1200 | CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTAT |
| 음 성 | 961 1260 | TGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGGTCAACAGTGAGATGCAAAGTAA |
| 음 성 | 1021 1320 | GGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGAAATATTTCAT |
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                                                                                                                            CTTACATCGTTTCTGGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG
                                                                                                                                         CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG
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                                                                                TGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG
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RESULT 8 US-09-785-276A-25756 ; Sequence 25756, Ap

Application US/09785276A

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APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: MORADAN, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION NUMBER: G0/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: G0/183,319
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR PRILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: G0/207,454
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: G0/207,454
PRIOR APPLICATION NUMBER: G0/211,314
PRIOR APPLICATION NUMBER: G0/211,314
PRIOR PILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: G0/219,007
PRIOR PILING DATE: 2000-07-18
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Best Local Similarity 99.9
Matches 1080; Conservative
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Pred. No. 6.2e-299;
0; Mismatches 1;
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APPLICANT: MODAHAM, JOHN
ITTLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITTLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITTLE OF INVENTION: HUMAN PROSTATE CANCER
CURRENT SAPLICATION HUMAN PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PRILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FRASTSEQ for Windows Version 4.0
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; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8,
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-30042
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US-09-785-276A-30042
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Best Local Similarity
Matches 1080; Conserv
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ORGANISM: Homo sapiens
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ilarity 99.9%;
Conservative
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Pred. No. 6.2e-299;
0; Mismatches 1;
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RESULT 11 US-60-261-974-40

Sequence 40, Application US/60261974
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODIN
TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEF
FILE REFERENCE: CL001095-PROV

AND USES THEREOF

ENCODING HUMAN NUCLEAR

CURRENT APPLICATION NUMBER: US/60/261,974 CURRENT FILING DATE: 2001-01-17 NUMBER OF SEQ ID NOS: 237 SOFTWARE: PastSEQ for Windows Version 4. SEQ ID NO 40

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                                         GAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGAAATATTTCATTTA 1320
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SEQUENCE 234, Application US/60205423
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: ISOLATED HUMAN G-PROTEI
ITITLE OF INVENTION: RECEPTORS, NUCLEIC ACII
ITITLE OF INVENTION: PROTEINS, AND USES THER
FILE REFERENCE: CLO00563
CURRENT APPLICATION NUMBER: US/60/205,423
CURRENT FILING DATE: 2000-05-19
UNMEER OF SEQ ID NOS: 494
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 234
LENGTH: 8161
TYPE: DNA
ORGANISM: HUMAN
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RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN
PROTEINS, AND USES THEREOP
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99.8%; Pred. No. 1.9e-295;
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Sequence 235, Application US/60205423
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN
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ISOLATED HUMAN G-PROTEIN

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Search completed: January 30, 2003, 09:39:16 Job time : 3519 secs

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Perfect score:
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Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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1081
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| US-10-270-857-1 US-10-270-587-1 US-10-270-587-1 US-10-305-720-1456 US-10-305-720-1456 US-10-272-983-35 US-10-264-237-1352 US-10-311-671-20 US-10-311-671-20 US-10-305-720-1482 US-09-461-436B-47 US-10-305-720-1108 US-09-461-436B-57 US-10-152-319A-2045 US-10-278-107-35 US-10-321-807-13 US-10-321-807-13 US-10-321-807-87 US-10-321-807-87 US-10-321-807-87 | US-10-017-161-525 US-10-270-144-3 US-10-270-144-1 US-10-188-405-7 US-10-321-807-27 US-10-278-141-10 US-10-278-107-33 US-10-278-107-33 US-10-296-081-10 US-10-296-774-102 | ID |
| 1, 12, 14, 14, 14, 14, 14, 14, 14, 14, 14, 14 | Sequence 525, Appli Sequence 3, Appli Sequence 1, Appli Sequence 7, Appli Sequence 70, Appl Sequence 10, Appl Sequence 33, Appl Sequence 10, Appl Sequence 10, Appl | Description |

| 45 | 44 | 43 | . 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 22 | 28 | 27 |
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| 83.8 | 83.8 | 84 | 84 | 84 | 84 | 84 | 84 | 84 | 87.2 | 87.6 | 87.6 | 87.6 | 87.6 | 90.4 | 90.8 | 90.8 | 90.8 | 93.6 |
| 7.8 | 7.8 | 7.8 | 7.8 | 7.8 | 7.8 | 7.8 | 7.8 | 7.8 | 8.1 | 8.1 | 8.1 | 8.1 | 8.1 | 8.4 | 8.4 | 8.4 | 8.4 | 8.7 |
| 1451 | 1451 | 1679 | 1679 | .1679 | 1670 | 1225 | 1059 | 1059 | 2409 | 8367 | 5015 | 1192 | 1092 | 1922 | 2070 | 2070 | 1900 | 2807 |
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| US-09-360-482B-19 | US-09-958-805A-1 | US-10-325-899-9205 | US-10-170-385-332 | PCT-US02-04915-80 | US-60-427-982-317 | US-10-305-720-1235 | US-10-245-882-46 | PCT-US02-29560-46 | US-09-360-482B-21 | US-10-017-161-807 | US-10-017-161-765 | US-10-017-161-511 | US-10-321-807-35 | US-10-152-319A-2068 | US-10-245-882-44 | PCT-US02-29560-44 | US-10-305-720-1484 | US-09-979-603-1 |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | | | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| 19, Appl | 1, Appli | 9205, Ap | | 80, Appl | 317, App | | | 46, Appl | 21, Appl | | 765, App | ٠ | 35, Appl | m | 44, Appl | 44, Appl | 1484, Ap | 1, Appli |

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; NAME/KEY: CDS
; LOCATION: (201)..(1214)
US-10-017-161-525
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US-10-017-161-525
j. Sequence 525, Application US/10017161
j. GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 1081; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLB OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
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CURRENT FILING DATE: 2002-12-18
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LOCATION: (1)..(
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241 GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC 300
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                                                                                 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA 240
                                                                                                                                                                                                               AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCTTTTGGAA
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                                         AATGCAGTAGTGATATCCACTTACATTTTCAAAATGA 387
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Pred. No. 8.4e-295;
); Mismatches 0;
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US-10-270-144-1
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GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1014
TYPE: DNA
ORGANISM: Human
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              TGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATT 533
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                                                        ATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGC
                                                                          ATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGC
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CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGGATCATT
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GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long

APPLICANT: Zhao, Jiagang

APPLICANT: Zhao, Jiagang

APPLICANT: Tularik Inc.

TITLE OF INVENTION: Novel Receptors

FILE REFERENCE: 018781-008410US

CURRENT APPLICATION NUMBER: US/10/188,405

CURRENT FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: US 60/302,800

PRIOR TILING DATE: 2001-07-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

LENGTH: 1014

TYPE: DNA

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                                                                                                                                                                   ORGANISM: Homo sapiens
FEATURE;
OTHER INFORMATION: human TGR164
US-10-188-405-7
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TAAGCGGGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA 1014
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                                                                                                                                  Length 1014;
                                                                                                         Indels
                                                                                                       0,
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APPLICANT: REDDY, ROOPA
APPLICANT: KALLICK, Deborah A.
APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096 USA
CURRENT APPLICATION NUMBER: US/10/278,141
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/208,834
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US01/16285
PRIOR APPLICATION NUMBER: 60/207,566
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/205,628
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR APPLICATION NUMBER: 60/208,222
PRIOR APPLICATION NUMBER: 60/206,222
PRIOR APPLICATION NUMBER: 60/206,222
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL PROGram
LENGTH: 1014
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US-10-278-141-10
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GENERAL INFORMATION:
APPLICANT: PATTERSON, Chandra
APPLICANT: LU, Dyung Aina M.
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ELLIOTT, Vicki S.
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KHAN, Farrah A.
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LU, Dyung Aina M.
THORNTON, Michael
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; ORGANISM: Homo sapiens
; FEATURE;
; MAME/KEY: misc_feature
; OTHER INFORMATION: Incyt
US-10-278-141-10
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Pred. No. 1.7e-275;
0; Mismatches 1;
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APPLICANT: AU YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0996 PCT
CURRENT APPLICATION NUMBER: US/10/296,081
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/205,628; 60/207,566; 60/208,834; 60/208,861
PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-06-02; 2000-06-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
SOFTWARE: PERL Program
FILING 104
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6575963CB1
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594 TCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTG
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KALLICK, Deborah A.
TANG, Y. Tom
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BLLIOTT, Vicki S.
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KHAN, Farrah A.
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PRIOR APPLICATION UNMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SEQ ID NO 102
FEROM: 545
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAMES/KEY: misc_feature
LOCATION: (1)...(545)
OTHER INFORMATION: n = a,t,c or g
US-10-276-774-102
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US-10-276-774-102/c
; Sequence 102, Application US/10276774
; GENERAL INFORMATION:
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Matches
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
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                                                        TCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCG 382
TCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCG
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                                                                                                                             Conservative
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98.7%;
                                                                                                                     Score 479.8; DB 6;
Pred. No. 2e-125;
0; Mismatches 2;
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RESULT 12
US-10-305-720-1456
US-10-305-720-1456
; Sequence 1456, Application US/10305720
; GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OP INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
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                                                              CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGRAM
SQUID NO 1456
LENGTH: 3055
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RESULT 13
US-10-272-983-35
; Sequence 35, Application
; GENERAL INFORMATION:
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; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No: g798835
US-10-305-720-1456
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Pred. No. 1e-27;
0; Mismatches 408;
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US/10272983

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Sequence 20, Application US/10311671 GENERAL INFORMATION:
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                                                            INVENTION: G-PROTEIN COUPLED RECEPTORS
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SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 1542
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME OF SEQ ID NO 20
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; OTHER INFORMATION: Incyte ID No: 3485895CB1
US-10-311-671-20
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PRIOR APPLICATION NUMBER: PCT/US01/19275
PRIOR APPLICATION NUMBER: PCT/US01/19275
PRIOR APPLICATION NUMBER: PCT/US01/19275
PRIOR APPLICATION NUMBER: 60/212,483
PRIOR PILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 60/215,209
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,595
PRIOR APPLICATION NUMBER: 60/216,936
PRIOR APPLICATION NUMBER: 60/218,936
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Best Local Similarity 49.3%;
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                                                                                                                                                                                                                                                                                    528 AȚCAȚTTCĄCTGGȚĄGCTGȚCAȚTÇCGĄTGACCTTÇTȚGĄȚCĄCATÇAACCAACAGGACÇ
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                                                   AACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTAT 707
                                                                                                                                                                     ААСАGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTAC
                                                                                                               AATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACTACAACCTCATTTAC
AGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTTGTGATGTGTTTTCTTTAT
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Pred. No. 5.8e-27;
0; Mismatches 433
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RESULT 15 US-10-311-671-20

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

LAL, Preeti G.
BAUGHN, Mariah R.
HAFALIA, April J. A.
NGUYEN, Danniel B. INCYTE GENOMICS, INC.

APPLICANT: APPLICANT: APPLICANT:

GRAUL, KILLERYAO, Monique G.

CHAWLA, Narinder

APPLICANT:

APPLICANT

ARVIZU, Chandra S. LU, Dyung Aina M. TRIBOULEY, Catherine

3

APPLICANT

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Henry Farrah A.

APPLICANT: APPLICANT: APPLICANT:

GANDHI, Ameena R. KALLICK, Deborah A. GRIFFIN, Jennifer A.

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

HERNANDEZ, Roberto WALSH, Roderick T. BOROWSKY, Mark L. THORNTON, Michael B

818

RAMKUMAR, Jayalaxmi AU-YOUNG, Janice K. ELLIOTT, Vicki S.

APPLICANT:

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| | Search completed: January 30, 2003, 07:08:00 Job time : 916 secs | Joj. |
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| | y 936 ACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTT 979 | Æ |
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JS-10-272-983-35
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CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILLING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILLING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILLING DATE: 1999-02-16
PRIOR FILLING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILLING DATE: 1999-02-26
PRIOR FILLING DATE: 1999-02-26
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LENGTH: 1005
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Best Local Similarity
Matches 436; Conserv
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SOFTWARE: PatentIn Ver. 2.1
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PRIOR FILING DATE: 1999-05-8
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
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                                                                                                                                  ATGAGCTGCTTTTCCATAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGG 527
                                                                                                                                                                                                                             AGCAGCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCA 467
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  GTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCCTTATAAATCCTGTTATAACTGAC
                                             ACCAGCATTCTCTTTCTCACTTTTATCÄGCATAGATCGATACTTGATAATTÄAGTÄTCCT 381
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Pred. No. 5e-27;
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 1352
LENGTH: 1436
TYPE: DNA
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US-10-264-237-1352
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA131P1
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TGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTCATGCCAACCTCTAT
                                      TGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTAT 407
                                                                                 GACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTTATGCCAATGG---AAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 131.2; DB 6;
Pred. No. 5.7e-27;
0; Mismatches 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
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TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/270,857
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 09/908,593
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR PRILING DATE: 1997-01-10
PRIOR PILING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESULT 10
JS-10-270-857-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity, 49:
Matches 438; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Human G-Protein Coupled Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1428
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AGCAGCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCA 467
                                          TGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTCATGCCAACCTCTAT
                                                                                   TGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTAT 407
                                                                                                                            GACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTTATGCCAATGG---AAAC 352
                                                                                                                                                                   GATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAAAC 347
                                                                                                                                                                                                              ATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCTTTAACCTCTCTGTCTCT 295
                                                                                                                                                                                                                                                  ATTITICAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACA 287
                                                                                                                                                                                                                                                                                               TTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCATTGTTGTTTACGGCTAC
                                                                                                                                                                                                                                                                                                                         ATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTAC 227
                                                                                                                                                                                                                                                                                                                                                                               GCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAAAGTACTACCTTTCCATT 175
                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAACCATTCTGCTACTC 794
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CURRENT APPLICATION NUMBER: US/10/270,587
CURRENT APPLICATION NUMBER: US/9/908,593
PRIOR APPLICATION NUMBER: US 09/908,593
PRIOR FILLING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR PILLING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR FILLING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
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US-10-270-587-1
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                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                  Matches
                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human G-Protein Coupled Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PF217C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Li, Yi
                                                                                                                                                                                                                                                                   LENGTH: 1428
TYPE: DNA
ORGANISM: Homo sapiens
                                                                            116
168 ATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTAC 227
                                                                                                             108 GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   708 ACCACGATT-----ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG
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                                                                    GCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAAAGTACTACCTTTCCATT 175
                                                                                                                                                                438; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGG 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCACTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTGTGGCCCTTTCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAAC 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICCATATOTIGAGGGICATICGGATCGAATCICGCCTGCTTTCAATCA-----GTIGI 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCATGTGTCTAACACTGTTGGGGGTTCCTTATTCCTCTTTTTGTGATGTGTTTCTTTTAT
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                                                                                                                                                                                                                                                                                                                                                           version 3.1
                                                                                                                                                                                  12.4%;
                                                                                                                                                         Score 134.4; DB 6;
Pred. No. 7.1e-28;
0; Mismatches 431;
                                                                                                                                                            Indels
                                                                                                                                                                                                   Length 1428;
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RESULT 7
US-10-278-107-33
                                                                                                                                                                               TYPE: DNA
ORGANISM: HOMO SAPIENS
(S-10-278-107-33
                                                                                                                                                                                                                               SOFTWARE: Fast
SEQ ID NO 33
LENGTH: 1014
                                                                                                           Query Match
Best Local Similarity
Matches 1013; Conserv
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PRIOR APPLICATION NUMBER: US/10/125,749
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US/09/988,922
PRIOR APPLICATION NUMBER: US/09/988,922
PRIOR FILING DATE: 2001-11-19
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                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 82
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CURRENT APPLICATION NUMBER: US/10/278,107
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: EVE Mahe
TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
TOTLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
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APPLICANT: Yuan Zhu
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     GTAAGCGGGAACCTTGAGCAAGCAAGAAAATTAGTTACTCAAACAACCCTTGA 1067
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Joyce Yue Mao
Wendy S. Halsey
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George H. Poste
Michel Louis Souchet
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John W. Quillen, Jr.
Erin M. Toland
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Melanie Robbins
David Malcolm Duckworth
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Stephane Clement Krief
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander Taylor
Henry Sarau
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Catherine E. Ellis
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Randall Forrest Smith
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Nabil A. Elshourbagy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han Ngoc Trinh
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Philip Graham Szekeres
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                                                                                                             Conservative
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Sequence 10, Application US/10296081
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: PATTERSON, Chandra
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Yan
APPLICANT: LU, Yan
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(S-10-321-807-27)
Sequence 27, Application US/10321807
SENERAL INFORMATION:
APPLICANT: Chen, Rupong
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: Non-Endogenous, Co
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REFERENCE: ARENOO86
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SOSTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
US-10-321-807-27
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/09/714,008
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,088
PRIOR APPLICATION NUMBER: 60/166,088
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PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,901
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,900
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR APPLICATION NUMBER: 60/181,749
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APPLICATION NUMBER: 60/166,369
FILING DATE: 1999-11-17
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Sequence 3, Application US/10270144
GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750CON
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR PILING DATE: 2000-05-18
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; ORGANISM: Human
US-10-270-144-3
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 9905
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Sequence 236, Application US/60205423

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
ITITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENC.
ITITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000563

CURRENT APPLICATION NUMBER: US/60/205,423

CURRENT APPLICATION NUMBER: US/60/205,423

CURRENT FILLING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 494

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 236

LENGTH: 8161

TYPE: DNA
COENTIEM: NUMBER
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; LENGTH: 43262
; TYPE: DNA
; ORGANISM: Human
US-60-261-974-40
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CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG 960
                                                          TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
                                                                                                                 CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA
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US-60-205-423-233

US-60-205-423-233

Sequence 233, Application US/60205423

Sequence 233, Application US/60205423

SERERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL000563

CURRENT FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 494

SOPTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 233

LENGTH: 8161

TYPE: DNA

ORGANISM: HUMAN
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CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGGTGGTGGATCATTTCACTGG 540
                                                                                     TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT
                                                                                                      TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT 480
                                                                                                                                             ATTTCATGTGTAAGCTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT 420
                                                                                                                                                                                                                     TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTCGAG 360
                                                                                                                                                                                                                                                            GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC 3667
                                                                                                                                                                                                                                                                              GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC 300
                           CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGGATCATTTCACTGG
                                                                                                                                                                                                        TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG
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FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: HUMAN PROSTATE CANCER
                                                                     SEQ ID NO 29927
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo (
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; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 4, E
; OTHER INFORMATION: n =
US-09-785-276A-29927
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Matches 1080; Conservative
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            CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTTGGTAACCTGTTACTATATG
                                               TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
                                                            TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
                                                                                              CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTACCCTTTCCATATCTTGAGGGTCA
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99.9%; Pred. No. 6.2e-299;
vative 0; Mismatches 1;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1307)
US-09-475-790-2
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SEQ ID NO 2
LENGTH: 1729
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Best Local Similarity
Matches 1080; Conserv
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TITLE OF INVENTION: Novel Seven-Transmembrane
TITLE OF INVENTION: Proteins/G-Protein Coupled Receptors
FILE REFERENCE: 5800-67
CURRENT APPLICATION NUMBER: US/09/475,790
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 34
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99.9%; Pred. No. 6.2e-299;
Live 0; Mismatches 1;
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Sequence 24015, Application US/09785276A

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: MORADAN, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: HUMAN PROSTATE CANCER
FITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/27,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
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; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9,
OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-24015
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOPTWARE: PastSEQ for Windows Version
SEQ ID NO 24015
LENGTH: 1729
TYPE: DNA
                                                                                                                                        Query Match 99.9%;
Best Local Similarity 99.9%;
Matches 1080; Conservative
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                      AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCTTTTGGAA 120
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                                                                                                                                        Score 1079.4; DB 30;
Pred. No. 6.2e-299;
0; Mismatches 1; 1
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Sequence 3, Application US/09634656
GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750
CURRENT APPLICATION NUMBER: US/09/634,656
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR PILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 9905
TYPE: DNA
ORGANISM: Human
US-09-634-656-3
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                                                          Query Match 100:0%; Score 1081; DB 24; Length 9905; Best Local Similarity 100.0%; Pred. No. 4.9e-299; Matches 1081; Conservative 0; Mismatches 0; Indels 0;
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1 CATATTGCCAAACTGAACTCTCTTGTTTTCTTGCAAGATGAAAGGAGACAACCATGAATG 60
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; LENGTH: 1081
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(1064)
US-10-010-568-1
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US-10-010-568-1
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY23, EXPRESSED ]
TITLE OF INVENTION: KIDNEY
FILE REFERENCE: DOOT? NP
FULE REFERENCE: DOOT? NP
CURRENT APPLICATION NUMBER: US/10/010,568
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/251,926
PRIOR APPLICATION NUMBER: US 60/269,795
PRIOR APPLICATION NUMBER: US 60/269,795
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.0
LENGTH: 1081
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Best Local Similarity
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US-60-200-364-53
US-60-200-364-54
US-60-200-364-54
US-60-311-340-1
US-09-634-656-1
US-09-985-453-2
US-09-985-453-2
US-09-985-453-27
US-09-985-453-27
US-09-985-453-27
US-09-985-333-13
US-10-096-511-25-973
US-09-988-922-333
US-10-023-7758-1
US-09-989-922-33
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Sequence 1, Application US/60251926
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COI
TITLE OF INVENTION: KIDNEY
FILE REFERENCE: D0077 PSP
CURRENT APPLICATION NUMBER: US/60/251,926
CURRENT FILING DATE: 2000-12-07
JEMNYMEERSOF SEQ ID NOS: 35
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PRIOR APPLICATION NUMBER: UK 0021484.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 2051
TYPE: DNA
ORGANISM: Homo sapiens
IS-09-944-807-20
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JS-09-944-807-20

Sequence 20, Application US/09944807

Patent No. US200220119494A1
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                                                                                                      Query Match 7.7%;
Best Local Similarity 52.0%;
Matches 186; Conservative
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SEQ ID NO 218
LENGTH: 2051
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Best Local Similarity 52.0%;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method for identifying substances which positively TITLE OF INVENTION: influence inflammatory conditions of chronic TITLE OF INVENTION: inflammatory airway diseases FILE REFERENCE: 082 00n CURRENT APPLICATION NUMBER: US/09/944,807 CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
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                                      183 TTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTTACATTTTCAAAATGAGA 242
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TTTATCTTTGGGCTTCTGGGCAATGGCCTTGCCCTGTGGATTTTCTGTTTTCCACCTCAAG 231
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                                                                                                    Score 82.8; DB 10;
Pred. No. 2e-14;
0; Mismatches 172;
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Search completed: January 30, 2003, 06:50:14

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FEATURE:

NAME/KEY: CDS

LOCATION: (232)...(1272)

NAME/KEY: misc_feature

LOCATION: (1)...(1700)

OTHER INFORMATION: n = a,t,c or
US-09-728-952-26
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JS-09-788-133-1
                                        . LOCATION: (1)..(1020) 
JS-09-788-133-1
                                                                                                                                                                                      CURRENT APPLIATION NUMBER: US/09/788,133
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 799

CURRENT PILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 101

SOFTWARE: pt_FL_genes Version 2.0

SEQ ID NO 26

SEQ ID NO 26
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Best Local Similarity
Matches 207; Conserv
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09788133 Patent No. US20020052001A1
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   FILE REFERENCE: P79011
                                                                                                                                                                                                                                                                                                                    APPLICANT: GLAXO GROUP LTD TITLE OF INVENTION: ASSAY
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                                                                                   FEATURE:
NAME/KEY: CDS
                                                                                                                              TYPE: DNA
ORGANISM: homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTACTATGCCAGTGGCGAAAACTGGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATGCTGAACCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCT 697
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                                                                                                                                                                         1020
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  8.4%;
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Pred. No. 1.1e-17;
  Score 90.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733
  DB 10;
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Length 1020;
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                                                                                            SOFTWARE: PatentIn
SEQ ID NO 2143
LENGTH: 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2143, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                            APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Horne, Darci T. APPLICANT: Vockley, Josep
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                               TYPE: DNA
                     ORGANISM: Homo sapiens FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 CTGGTCCTGCCCACCCGCCTGGTCTACCACTTCTCTGGGAACCACTGGCCATTTGGGGAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATC 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCCTGCGGCAGGGCCTGCGTGTGGAGAAGCGCCTCAAGACCAAGGCAGTGCGCATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAACC 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGTCATTCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACAGATCAGCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCACCTGCATCAGCGCCGACCGTTTCCTGGCCATTGTGCACCCGGTCAAGTCCCTCAAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACCTGTTTCAGCATCTTCCGCTACTGTGATCATTCACCCAATGAGCTGCTTTTCC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTC 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATCTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTATCCTGGCTTTAGTTGGCAATACCCTGGCTCTGTGGCTTTTCATCCGAGACCACAAG 183
                                                                                                                                                                                                                                                                                                                                                                                              Vockley, Joseph
Scherf, Uwe
                                                                                                                                             Ver.
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RESULT 6
US-09-828-478-1
                                                                                                                         FILE REFERENCE: 04974.00458

CURRENT APPLICATION NUMBER: US/09/828,478

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 60/195,196

PRIOR FILING DATE: 2000-04-07

PRIOR PPLICATION NUMBER: 60/254,876

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 16
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CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-19
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-791-1
TYPE: DNA
ORGANISM: Homo sapiens
:-09-828-478-1
                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09828478 Patent No. US20020155528A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pfizer Inc
TITLE OF INVENTION: No. US20010039037A1el Polypeptide
FILE REFERENCE: PC10914ADAM
                                                                   LENGTH: 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATIGCTGAACCTIGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207;
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52.3%;
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Pred. No. 8.5e-18;
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GENERAL INFORMATION:

APPLICANT: Pfizer Inc.

TITLE OF INVENTION: NO. US20010039037A1el Polypeptide

FILE REFERENCE: PC10914ADAM

CURRENT APPLICATION NUMBER: US/09/826,791

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 0008504.3

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: 60/198,367

PRIOR PILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 6

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Matches 207; Conserv
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Patent No. US20010039037A1
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TCATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCC
                    TTATGCTGAACCTGGCCCTGCACAGATCTGCTGTTATCTGACCAGCCTCCCCTTCCTGATTC 324
                                                                  ATGGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTT
                                                                                                     ATGCAGTAGTGATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCA 264
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Pred. No. 8.7e-18;
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Pred. No. 8.7e-18;
0; Mismatches 189;
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Sequence 1, Application US/09943798
Patent No. US20020065215A1

GENERAL INFORMATION:
APPLICANT: GLAXO Group Limited
TITLE OF INVENTION: Polypeptide
PILE REFERENCE: QG1021
CURRENT APPLICATION NUMBER: US/09/943,798
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 831
TYPE: DNA
ORGANISM: Homo sapiens
(S-09-943-798-1
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                                                Conservative
                                          76.9%; Score 831; DB 10; Length 100.0%; Pred. No. 1.6e-236; tive 0; Mismatches 0; Indels
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           AGCGGGAACCTTGAGCAAGCAAGAAAATTAGTTACTCAAACAACCCTTGA 1067
                                             TATGTGGTGGTCAGCAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTA
                                                           TATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTA 1016
                                                                                               GAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTTGGTAACCTGTTACTA
                                                                                                            GAAGCITACATCGITICTAGACCATTAGCIGCTCTGÀACACCTTTGGIAACCIGTTACIA 956
                                                                                                                                                GTCATTCGGATCGGATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCAT
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020128187A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 787CIP2F
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-728-422-1
                                                                                                                                                                                                                                                                           Sequence 1, Application US/09728422
Patent No. US20020128187A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
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JS-08-472-840-60
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Patent No. 5763575
.GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
                                                                                                                             Query-Match 9.0%; Score 97.8; DB 1; Length 2 Best Local Similarity 52.6%; Pred. No. 6e-20; Matches 213; Conservative 0; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
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ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
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PRIOR APPLICATION NUMBER: US/08/390,301
APPLICATION NUMBER: US/08/390,301
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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ADDRESSEE: MORRISON & FOERSTER
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                                            295 CTGÁCCÁCGGTCTTTCTTCCGGTCGTCTACATTATTGTGTTTTGTGATTGGTTTTGCCCAGT 354
                                                                                144 CTCAAGATGCACTACCTCCCTGTTATTTATGGCATTATCTTCCTGGGGGATTTCCAGGC 203
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655
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GGCGTCTCCTTGGCAATCTGGCTCCTGATTTTTCTGGTCACCATC
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Search completed: January 30, 2003, 06:48:46
Job time: 78 secs

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LOCATION:
US-08-476-976-1
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Best Local Similarity 52...
213; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: SUNDEL
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APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REGISTRATION NUMBER: 30,988
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NAME/KEY:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                           562 TACATGGCCAACCTGGCCTTGGCCGACCTCCTCTCTGTCATCTGGTTCCCCCCTGAAGATC 621
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                                384 TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTC 443
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/476,976
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                                                                           TCCTACCACCTACATGGCAACAACTGGGTCTACGGGGAGGCCCTGTGCAAGGTGCTCATT 681
                                                                                                                  CACTACTATECCAGIEGCEAAAACTEGATCTTTEGAGATTTCATETTAAGTTTATCCEC 383
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VENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
VENTION: AND ANTAGONISTS, AND NUCLBIC ACIDS ENCODING THE RECEPTOR
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CTATGGTAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAG 741
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Pred. No. 4.3e-20;
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US-08-474-410-1
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Best Local Similarity
Matches 213; Conserv
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FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pair
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NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,
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APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1995
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCARBOROÚGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                              204 AATGCAGTAGTGATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATC
                                                                                               442 CIGACCACGGTCTTTCTTCCGGTCGTCTACATTATTGTGTTTTGTGATTGGTTTTGCCCAGT 501
                                                                                                                               144 CTCAAGATGCACTACCTCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGC 203
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264 ATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATT 323
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                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                AATGGCATGGCCCTCTGGATCTTCCCTTTTCCGAACGAAGAAGAAACACCCCGCCGTGATT 561
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232..1416
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232
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                                                                                                                                                                                   Score 97.8; DB 3;
Pred. No. 4.3e-20;
                                                                                                                                                                     Mismatches 192;
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Patent No. 5629174
GENERAL INFORMATION:
APPLICANT: SUNDELIN
APPLICANT: SCARBORG
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Best Local Similarity 57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 200;
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                                                                                                                                                               ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
                                                                                                                                                  CURRENT APPLICATION DATA:
                                                        ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
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                                                                                         APPLICATION NUMBER: FILING DATE: 26-JUI CLASSIFICATION: 43
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TOPOLOGY: 111
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LOCATION: 28..1011
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DEDNESS: double
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US-08-097-938-1
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Best Local Similarity
Matches 213; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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NAME/KEY:
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NAME/KEY:
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                                                                                                                                                                                               CITY:
 APPLICATION NUMBER:
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TYPE: nucleic acid
STRANDEDNESS: single
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MATION:
MEDICIN, JOHAN
SCARBOROUGH, ROBERT M.
SCARBOROUGH, ROBERT M.
SCARBOROUGH, RECOMBINANT C140 RECEPTOR, ITS AGONISTS
AVENTION: RECOMBINANT C140 RECEPTOR ACIDS ENCODING THE RECEPTOR
                                                                                                                                                         USA
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Pred. No. 4.3e-20;
0; Mismatches 192;
                                                                                                                                                                                                             Ste. 5500
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RESULT 5
US-08-446-088A-1
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                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,088A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08446088A Patent No. 5691156
 TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT:
APPLICANT:
                                                                       NAME: Kenneth D. Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                     ZIP: 28234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCT 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GÉTGTGTCTGATGCACTGTATGCGGCCTCCCTGCCGCTGGTCTATTACTACGCCCGC 341
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                                                                                                                                                                                                                                                                                                                                                                               Charlotte
No. 5691156th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                       Post Office Drawer
1842 base pairs
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Harden, Thomas K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parr, Claude E.
Sullivan, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weisman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boucher, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laura
                                                                                                                                                                                                                                                                                                                                                                                                                   Seltzer, Park & Gibson
ice Drawer 34009
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US-08-513-974B-41
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Best Local Similarity 52.9%;
Matches 222; Conservative
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                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                           APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                APPLICANT:
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FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
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                                                                                                                                          COUNTRY: US
ZIP: 02109
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                                                                                                                                                                                                                       ADDRESSEE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                    Boston
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                                                                                                                                                                                                    130 Water Street
                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                             Fujii, Ryo
Ohtaki, Tetsuya
Fukusumi, Shoji
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                                                                                                                                                                                                                                                                                                                                                                         Hinuma, Shuji
                                                                                                                                                                                                            DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-749-707-1
                                                                                                                                                                                                                                                                             Sequence 1, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC INVENTION: 14
COUNTRY: USA
ZIP: 20036-5869
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
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1800 M Street, N.W.
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US-08-749-707-1
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Best Local :
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEPHX: 202-467-7176
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NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 11.9%;
Local Similarity 50.1%;
hes 380; Conservative
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GAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTGTGCTTTTTACACCC
                                    CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTACCC
                                                                          TACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAGGTTGCTACTGCTCTGCCCCCTT 1305
                                                                                                                                                         AGCATGTGTCTAACACTGTTGGGGGTTCCTTATTCCTCTTTTTGTGATGTGTTTCTTTTAT
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                                                                                                                     ACCACGATT----ATCCACACTCTGACCCCATGGACTGCAAACTGACAGCTGCCTTAAG
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Pred. No. 1.4e-29;
0; Mismatches 370;
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                                           GCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCA 459
                                                                                                               CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 371
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                                                                                                                                                                                                                                                                                                                                                                                          TCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 291
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                                                                                                                                                                                                                            TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNs to prepare full-length cDNs libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Mateuura (Natahiki, M., Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA was cleaved with XhoI and SstI.
100 c 88 g 130 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Pred. No. 1.2e-17;
0; Mismatches 145;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                188 CTTTCTTCCGGTCGTCTACATTATTGTGTTTGTGATTGGTTTGCCCCAGTAATGGCATGGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                           155 CTACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGT 214
455 GATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTG
                                            428
                                                                                                                                                                                                                                                                                                             248 CCTCTGGATCTTTCCCGAACGAAGAAGAAACACCCCGCCGTGATTTACATGGCCAA
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                                                                                                                                                                                                                                                              ccrescerecacacacacrescereces consecreces consecreces consecrated 334
                                          TGGCAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAGAGGTACTGGGT
                                                                   TTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTTCAGCATCTTCCGCTACTGTGT 454
                                                                                                                                ACATGGCAACAACTGGGTCTATGGGGAGGCCCTGTGCAAGGTGCTCATTGGCTTTTTCTA
                                                                                                                                                                                                                     CCTGGCCTTGGCTGACCTCCTCTCTGTCATCTGGTTCCCCCCTGGCCATTGCCTACCACCT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence start: 25 High quality sequence stop: 799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 801)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sa
Site 2: Not1; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
228 c 193 g 213 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'clone lib="NCI_CGAP_Mam6"
'sex="female, virgin"
'tissue_type="infiltrating ductal carcinoma"
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strain="FVB/N"
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lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99.6; DB 13; Length 801; Pred. No. 2e-17; O; Mismatches 184; Indels 0
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nes 233; Conserv
                                   TGGTGTGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCA 579
                                                                                                                               TTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTG 519
                                                                                                                                                                                                                                                                                                           GCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCA 399
TIGIGIGGGIGCIGGIGCIGCCAGGCACCCGIGCICIACTICGICACCACCAGCG 1009
                                                                                         TGCGCCCTCTGCACTCCCTGCGTTGGGGCCCGGGTTATGCCCGCCGGGTGGCTGCGG
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                                                                                                                                                                                                                                                                GTGACCACTGGCCATTTAGCACGGTGCTCTGCAAGCTGGTGCGTTTCCTCTTCTACACCA
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/ Codon start=1
/ proteIn id="BAB30719.1"
/ proteIn id="BAB30719.1"
/ db_xref="MGI:12856589"
/ db_xref="MGD:MGI:105107"
/ db_xref="MGD:MGI:105107"
/ translation="MAADLEPWNSTINGTWEGDELGYKCRFNEDFKYVLLPVSYGVVC
/ translation="MAADLEPWNSTINGTWEGDELGYKCRFNEDKYVYYYZARGDHWPFS
TVLCKLLWFLFYTNLYCSILFIFICISVHRCLGVLFPLHSIRWGRARYARRVAVVVVL
VLACQAPVLYFVTSVRGTRITCHDTSAAELFSHFVAYSSVMLGLLFAVPFSVILVCY
VLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHLTRTLYYSFRSLDL
SCHTLMAINMAYKITRPLASANSCLDFVLYFLAGGRLVRFARDAKPPTEPTPSPQARR
KLGLHRPNRTVRKDLSVSSDDSRRTESTPAGSETKDIRL"
737 c 705 g 582 t 1 others
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484. .1605
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/note="data_source:MGD, source key:MGI:105107
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/strain="C57BL/GJ"
/db_xref="FANTOM_DB:5430432J15"
/db_xref="MGD:MGT:1897121"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="6 days neonate"
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5 (bases 1 to 3001)
Adachi, J., Aizawa, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015C04:purinergic receptor P2Y, G-protein coupled 2, full insert sequence.

AKO05013
                                                                                                                                                                                           Wynshaw-Boris, A., and Hayashizaki, Y.
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                                                                                                                                 Nature 409
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Akahira, S.,

Akimura, T.,

Aono, H.,

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                                                                                                                                                                                                                                                             Roslin Libourn EH25 yrs, Roslin, Midlothian, EH25 yrs, Roslin, Midlothian, EH25 yrs, Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Fmail: frazer.murray@bbsrc.ac.uk
Fmail: frazer.murray@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Frazer Murray
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                                                              /note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'
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163 c 125 g 108 t
                               /tissue_type="Brain"
/dev_stage="Unknown"
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                                                                                                                                                                                                                  organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 TCAAGATGCACTACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 TTATGCTGAACCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATTTTCCACGTGAACCTCTACGGCAGCATTCTGTTNCTCACGTGCATAAGCGTC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACTACTTCAACAAAACCGACTGGATCTTCGGGGACGTCATGTGCAAGCTGCAGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCAGTAGTGATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGTTCTACTACCTGCCCACCGTCTACATCCTCGTCTTCATCACCGGGTTCTTGGGCA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGCGTGGCCATCTGGATGTTCGTCTTCCACATGCGGCCGTGGAGCGGCATCTCGGTGT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI663305 mRNA
WA27610.yl Sugano mouse kidney mkia Mus
MAGE:1970226 5' similar to SW:P2YR_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T. Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., P., B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., R., E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                 MGI:986966
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Other_ESTs: uk27c10.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%;
Similarity 59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nouse mouse.
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                                                                                                                                                                                                                                                                                                                   quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                 /note="Organ: kidney; Vector: pME188-FL3; Site_1: DraIII (CACCATGTG'); Site_2: DraIII (CACCATGTG'); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                 /clone_lib="Sugano mouse
/sex="female"
                                                                                                                                                                                                              /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                             clone="IMAGE:1970226"
                                                                                                                                                                                                                                                        organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:4766888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                      490.
                                                                                                                                                                       kidney mkia"
[TGTTGGCCTACTGG], digested
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9 musculus cDNA (
F P49651 P2Y PUR:
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PURINOCEPTOR 1
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ACCESSION
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BG402029
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Best Local Similarity
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TITLE
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168 ATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTAC
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                                                                                                             GCAACTTGCAAAAACTGGCTGGCAGCAGAGGGCTGCCCTGGAAAAGTACTACCTTTCCATT 184
                                                                                                                                                                                               GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
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                                                                                                                                                                                                                                                                                                210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, In
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLCM1336 row: p column: High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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602466748F1 NIH_MGC_75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 877)
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             //Indian-World Will Minds (Clontech); Site 1:
//note= "Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
Sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGAGGCGGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.55
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE: 4594810"
/clone_lib="NIH MGC_75"
/lab_host="DH10B (TI phage=resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                    10.1%;
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                                                                                                                                                                                                                                                                             Score 109.4; DB 12;
Pred. No. 3.2e-20;
0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
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         188;
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BM4265
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Contact: Larry A. Cogburn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Project
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ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves; Neognathae;
Phasianinae; Gallus.
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         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cogburn@udel.edu, www
Location/Qualifiers
                                                                                                                                                              /notee"Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each developmental agg (across strains); Single pass sequencing from 5'-end" 223 c 210 g 121 t 7 others
                                                                                                                                                                                                                                                                                                                                                /tissue_type="Abdominal Fat"
/dev_stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pgf2n.pk002.o6"
/clone_lib="Normalized Chicken
                                                                                                                                                                                                                                                                                                  lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Gallus gallus"
|strain="Commercial broil
                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:9031"
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57.5%;
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                                    Pred. No. 4.2
Mismatches 139;
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                                       4.2e-20;
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145 TCAAGATGCACTACCTCCCTGTTATTTATGGCATTATCCTCGTGGGATTTCCAGGCA 204

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATATOTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257;
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archogauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                         mRNA sequence.
BQ038875
BQ038875.2 GI:20383637
                                                                                                                                                                                                    BQ038875

B9911C.pk010.113 normalized chicken lymphoid cDNA library Gallus
gallus cDNA clone pgn1c.pk010.113 5' similar to
sp|P34996|P2YR CHICK P2Y PURINCCEPTOR 1 (ATP RECEPTOR) (P2Y1)
(PURINERGIC RECEPTOR) pir|S33733 G protein-coupled receptor chicken emb|CAA51716.1| (X73268) ATP receptor P2Y1 [Gallus gallus],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone Distribution: Researcherics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="fetal"
//dev stage="fetal"
//dev stage="fetal"
//lab_host="PHIOB (Life Technologies) (Tl phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UTE-EO1 is a normalized CDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA, synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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/clone_lib="UI-E-EO1"
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Pred. No. 8.4e-63;
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BQ396255

MISC ng19g07.y1 NICHD XGC Emb6 & IMAGE:5383884 5', mRNA sequence BQ396255

BQ396255

BQ396255.1 GI:21083932
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Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
On Mar 27, 2002 this sequence version replaced gi:19772415.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pgnic.pk010.113"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Pemale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="thymus, bursa,
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"
199 c 172 g 128 t
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RESULT 14
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                 Human;
                                                Human AXOR89 (G-protein coupled receptor) cDNA.
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AXOR89 polypeptide;
ion; cancer; pain; a:
                                                                                (first entry)
e; G-protein coupled asthma; Parkinson's
                                                                                                                                                  ВР
receptor; vaccine;
Disease; diabetes;
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Query Match Best Local Similarity Matches 1013;

93.7%;

Conservative

0;

Score 1012.4; DB 2 Pred. No. 8.5e-287; 0; Mismatches 1;

24; Length

1014; 0 Gaps

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54 ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCT 113

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ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCT

infection;

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293 180 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC

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The invention relates to an isolated AXOR89 polypeptide (G-protein CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide CC and polynucleotide encoding the polypeptide, is useful for identifying CC and polynucleotide (or inhibitors) that are potentially useful in treating conditions associated with an AXOR89 imbalance, such as CC bacterial, fungal or protozoan infections, cancers, pain, asthma, cC parkinson's Disease, diabetes, obesity, anorexia, bulinia, acute heart CC failure, hypotension, hypertension, urinary retention, osteoporosis, cangina pectoris, myocardial infarction, stroke, ulcers, allergies, benign CC prostatic hypertrophy, migraine, vonitting, psychotic and neurological CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia, CC dyskinesias, such as Huntington's Disease or Gilles dela Tourette's cyndrome. The polynucleotide sequence may also be used for chromosome CC localisation or tissue expression studies. The AXOR89 is used as a CC vaccine or to produce fusion proteins. The present sequence is human axona control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer; stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia; myocardial infarction; allergy; benign prostatic hypertrophy; migraine; vomitting, psychotic; neurological disorder; anxiety; manic depression; delirium; Huntington's Disease; Gilles dela Tourette's syndrome; dementia; dyskinesia; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel AXOR89 polypeptide and polynucleotide encoding it, useful for identifying agonists and antagonists in the treatment of diseases associated with an AXOR89 imbalance, such as cancers, diabetes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK )
  Sequence 1014 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                          AXOR89 cDNA.
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DB; AAE21803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            severe mental retardation, Huntington's disease and Tourette's syndrome. The present sequence encodes the P2Y1-like GPCR of the invention.
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               CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1013
                                                                   CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGTGAACACCTTTGGTAACCTGTTA 953
                                                                                                            AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                                         AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                                                                                  AGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTG
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100.0%; Pred. No. 2.9e-287;
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The present specifically claimed human cDNA sequence (located on CC chromosome 13) encodes a purinergic-related G-protein coupled receptor CC (GPCR) of the invention. GPCRs constitute a major class of proteins CC responsible for signal transduction within a cell. Upon binding of a CC ligand to the extracellular portion of a GPCR, a signal is transduced CC gPCR proteins can be divided into five families, family I contains the CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are CC characterised by their selective responsiveness towards ATP and its CR analogues, some also respond to UTP. The invention comprises a human CC g-protein coupled receptor protein and encoding nucleic acids. The GPCR CC protein and nucleic acids of the invention are useful in the treatment of the invention is useful for: the development/identification of the protein in biological fluids; identifying compounds which modulate of the protein in biological fluids; identifying compounds which modulate the activity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR nucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; CC controlling GPCR expression, and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated G-protein coupled receptor peptide useful for treating disorder characterised by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise antibodies.
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P-PSDB; AA014027.
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08-AUG-2000; 2000US-0634656.
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                   CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCCTTTGGTAACCTGTTA
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Pred. No. 2.9e-287;
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The invention relates to an isolated P2Y-like receptor polypeptide
CC (ABB83818-ABB83819) which is also referred to in the specification as
CC HIPHUM 0000037. An effective amount of a substance (agonist or
CC antagonist) which modulates P2Y receptor activity is useful to treat a
CC subject having a disorder that is responsive to P2Y-like receptor
CC modulation. The disorder that is responsive to P2Y-like receptor
CC prophylaxis of a disorder that is responsive to stimulation or modulation
CC prophylaxis of a disorder that is responsive to stimulation or modulation
CC of P2Y-like receptor activity. Disorders which may be treated include
CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
CC rihinitis, inflammatory pain and general inflammation such as tendonitis,
CC polymyositis or prostatitis. The invention provides alternative
CC substances for the treatment of immunological and inflammatory diseases.
CC The present sequence is that the P2Y-like receptor variant encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can used for the identification of agonists and antagonists which may be used to treat an immune or inflammatory disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000GB-0021524.
06-SEP-2000; 2000GB-0021894.
25-SEP-2000; 2000GB-0023444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulator; anti-inflammatory; cytostatic; antiasthmatic; gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide; antibacterial; immunosuppressive; dermatological; nephrotropic; antiallergic; analgesic; receptor; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Py2-like receptor; HIPHUM 0000037; immunity; cancer; Crohn's disease; irritable bowel syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P2Y-like receptor variant encoding gene
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CC (a) assessing whether a patient is afflicted with prostate cancer; CC (b) monitoring the progression of prostate cancer in a patient; CC (c) assessing the efficacy of a test compound to inhibit prostate CC cancer in a patient; CC (d) assessing the efficacy of a therapy for inhibiting prostate cCC (d) assessing the efficacy of a therapy for inhibiting prostate cancer CC in a patient; CC (e) selecting a composition for inhibiting prostate cancer CC (f) assessing the prostate cell carcinocer.

CC (f) assessing the prostate cell carcinocer.
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Best Local Similarity
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781, CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
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                                                                                   ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 780
                                                                                                                                                                   CTGCAACTACTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
                                                                                                                                                                                                         GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA
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                                       ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA
                                                                                                                                                                                                                                                                                        CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGGTGGGATCATTTCACTGG
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Pred. No. 2.3e-306;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 T; 17 other;
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etc., are used for diagnosis and (gene) therapy of diseases that are (in)directly associated with (I) or its expression products. No diseases are specified but as (I) is expressed only in thyroid tissue, (I) is presumed to be involved in regulation of thyroid function. The present

The invention relates to the human P2Y11i gene (I), including its 5' and 3' untranslated regions, located on chromosome 13 and encoding a G protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies

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RESULT 8
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                                                                                                                                                                                                                                                                                    New human P2Y11i gene, useful for treatment and diagnosis of associated diseases, and related proteins, antibodies and modulators, encodes G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; P2Y1-11; chromosome 13; G protein-coupled; receptor;
gene therapy; thyroid; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2002
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                                                                                                                                                                                                            Claim 5; Page 3; 5pp; German.
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(e) selecting
(f) assessing
(g) determinin
(h) assessing

    (a) assessing whether a patient is afflicted with prostate cancer;
    (b) monitoring the progression of prostate cancer in a patient;
    (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
    (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a parient;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0001-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 5175-5176; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACTGG
                                                                                                                                                                                                               ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
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 ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
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25-MAY-2000; 2000US-207454P.
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Novel isolated nucleic acid molecule associated with cancerous state of

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proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic analysis. The proteins and nucleic acids encoding them are useful for disgnosis and treatment of disorders selected from disorders of the spleen, lung such as Good pasture's syndrome, liver such as viral hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's disease, colon such as Crohn's disease, uterus and endometrium such as systemic lupus erythematosus, disease of the skin such as actinic keratosis, disorders of the heart such as myocarditis, disorders involving blood vessels such as Kawasaki syndrome, disorders involving the thymus such as DiGeorge syndrome, disorders involving B-cells such as poleoniasms, and disorders involving B-cells such as poleoniasms, and disorders of the breast such as inflammations, and disorders involving the testis and epididymis such as teratoma. Numérous examples of cach type of disorder are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.9%;
Best Local Similarity 99.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence encodes a novel human seven transmembrane domain protein belonging to the G-protein coupled receptor (GPCR) superfamily, protein 39404. The receptor is useful in drug screening assays, to identify compounds that modulate receptor activity and/or interact with the receptor, and for producing antibodies specific for the receptor, it regions or fragments. The receptor is useful for treating/diagnosing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;
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Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic pharmacogenomic marker; gene; ss.

Homo sapiens

23-AUG-2001

20-FEB-2001; 2001WO-US05171

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human P2Y1li gene, useful for treatment and diagnosis of associated diseases, and related proteins, antibodies and modulators, encodes G protein-coupled receptor -
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                  Zhao Q,
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2000US-0634656.
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RESULT 14
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                                           human.
Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
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Sequence 1
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G-protein coupled receptors purinoreceptor 1 (p2y1) Patent: EP 1219638-A 1 03-JU
                           Fidock, M.D.
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                                                                                       GI:21899357
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Patent EP1219638.
                                            Chordata;
Primates;
 03-JUL-2002,
                 having homology to the
                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA
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Pred. No. 6.9e-253;
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AB083598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-APR-2002) Shigeki Takeda, Gunma University, Department of Biological and Chemical, Engineering, Faculty Engineering; 1-5-1, Kiryu, Gunma 376-8515, Japan (E-mail:stakeda@bce.gunma-u.ac.jp, Tel:+81-277-30-1434,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1014)
Takeda,S., Kadowaki,S.,
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:+81-277-30-1434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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LVGFFGNAVVISTYIFKNEPWKSSTIIKLNLACTDLLYLTSLEPLIHYYASGINNIFG
DFMCKFIRFSFHFNLYSSILFLTCSSIFKYCUIHDMSCFSHKTRCAVVACAVVWI
SLVAVLEMTFLITSTNETURSACLDLTSSDELMTIKWYNLILTATTFCLFLVIVTVLCY
TTIIHTLTHGLQTDSCLKQKARRLTILLLLAFYVCFLFFHILRVIRIESRLLSISCSI
ENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted with SOSUI analysis"
/codon_start=1
/product="putative G-protein coupled receptor"
/protein_id="BAB89311.1"
/db_xref="GI:20152260"
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1014)

Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

Discovery and mapping of ten novel G protein-coupled receptor genes gene 275 (1), 83-91 (2001)
 2 (bases 1 to 1014)
Lee, D.K., Nguyen, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1014)
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AAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTG
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Sequence 1 from Patent W00187980.
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AX379468.1 GI:19575226
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                Applera Corporation Robert A. Millman Assistant Secretary Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             encoding human gpcr proteins, and uses thereof Patent: WO 0187980-A 1 22-NOV-2001;
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Beasley,E.M.
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100.0%; Pred. No. 2.7e-253;
tive 0; Mismatches 0;
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      26904, 38911, and 39404, seven-transmembrane coupled receptors
Patent: WO 0149847-A 2 12-JUL-2001;
                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1729)
Glucksmann,M.A. and White,D.
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/tranalation="museplbylanasdepdyaaafguctdeniplkwhylpviygiif
LVGFPGNAVVISTYIFKMRPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFG
DFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVVACAVVANII
SLVAVIFMTFLITSTNETNRSACLDLTSSDELNTIKWYNLILITATTFCLPLVIVTLCY
TTIIHTLTHGLOCDSCLUKGWARRLTILLLLAFYVCFLPFHILAVIRISSRLLSISCSI
ENQIHBAYIVSGPLAALNTFGNLLLYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYS
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AL356486
AL356486.12 GI:15808158
                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 67645)
Direct Submission
Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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On Sep 28, 2001 this sequence version replaced gi:15787734.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
database can be found at
http://www.sanger.ac.uk/Pordects/Colorat/organe/sanger.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/Pordects/Coloration.ac.uk/
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TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG
                                                                                                                                      GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
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/chromosome="13"
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be approximately 110bp by restriction digest data."
13252 c 13216 g 20635 t
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                              CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
                                                                                                                                         GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA
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CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
                                                                                                        GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA
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Patent: WO 0246414-A 1 13-JUN-2002;
Bristol-Myers Squibb Company (US)
Location/Qualifiers
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                                                                                                                                     AL Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.bDrc.jp/, Tel:81-3-359-8080, Pax:81-3-359-8081)
This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding (GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.
And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Crience Nivision, Research Center for Advanced Science and
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AB065877.1 GI:21929018
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Eukaryota; Metazoa;
                                                                                                         Science Division, Research Center for Advanced Technology (RCAST), University of Tokyo].

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/isolate="CBRC7TM 440"
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